

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 15:18:20 ; Search time 30.4494 Seconds
(without alignments)
2686.875 Million cell updates/sec

Title: US-09-301-507-74_COPY_1_50

Perfect score: 50

Sequence: 1 GCGTCGATCTTTTCTATGC.....GCGCCTATGGAGATACAG 50

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCITUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42.6	85.2	1878	4	US-09-620-312D-625
2	24.8	49.6	251769	4	US-09-949-016-13185
3	24.8	49.6	251769	4	US-09-949-016-13186
4	24.8	49.6	266748	4	US-09-949-016-13187
5	24.8	49.6	266748	4	US-09-949-016-13188
6	24.2	48.4	87190	4	US-09-949-016-16335
7	23.8	47.6	8044	4	US-09-949-016-16782
8	23.4	46.8	4403765	3	US-09-103-840A-2
9	23.4	46.8	4411529	3	US-09-103-840A-1
10	22.8	45.6	900	3	US-09-064-703-8
11	22.8	45.6	915	3	US-09-064-703-9
12	22.8	45.6	1590	3	US-09-064-703-1
13	22.8	45.6	1605	3	US-09-064-703-5
14	22.8	45.6	1701	3	US-09-064-703-4
15	22.8	45.6	35100	2	US-08-770-379-17
16	22.8	45.6	35100	3	US-08-757-669A-17
17	22.8	45.6	35100	3	US-09-230-371A-17
18	22.4	44.8	868	3	US-08-889-502-20
19	22.2	44.4	28555	4	US-09-949-016-13106
20	22.2	44.4	181251	4	US-09-949-016-15970
21	21.8	43.6	601	4	US-09-949-016-105635
22	21.8	43.6	601	4	US-09-949-016-105636
23	21.8	43.6	601	4	US-09-949-016-105637
24	21.8	43.6	129899	4	US-09-949-016-14684
25	21.8	43.6	148156	4	US-09-949-016-11776
26	21.8	43.6	228896	4	US-09-949-016-17127
27	21.6	43.2	601	4	US-09-949-016-177006

28	21.6	43.2	942	4	US-09-902-540-6941	Sequence 6941, App
29	21.6	43.2	1167	4	US-09-489-039A-2409	Sequence 2409, App
30	21.6	43.2	1895	3	US-09-326-203A-14	Sequence 14, Appl
31	21.6	43.2	1976	3	US-09-165-042-2	Sequence 600, App
32	21.6	43.2	4587	4	US-09-902-540-600	Sequence 16800, A
33	21.6	43.2	26896	4	US-09-949-016-16800	Sequence 132, App
34	21.6	43.2	35412	4	US-08-311-731A-132	Sequence 11980, A
35	21.6	43.2	125188	4	US-09-949-016-11980	Sequence 14624, A
36	21.6	43.2	147382	4	US-09-949-016-14624	Sequence 11930, A
37	21.6	43.2	325791	4	US-09-768-185A-1	Sequence 1, Appl
38	21.4	42.8	86947	4	US-09-949-016-11930	Sequence 59002, A
39	21.2	42.4	601	4	US-09-949-016-59002	Sequence 10, Appl
40	21.2	42.4	3000	4	US-10-007-010-10	Sequence 16286, A
41	21.2	42.4	53562	4	US-09-949-016-13453	Sequence 13501, A
42	21.2	42.4	119801	4	US-09-949-016-13453	Sequence 12541, A
43	21.2	42.4	128516	4	US-09-949-016-13501	
44	21.2	42.4	128516	4	US-09-949-016-13501	
45	21.2	42.4	133157	4	US-09-949-016-12541	

ALIGNMENTS

RESULT 1

US-09-620-312D-625

Sequence 625, Application US/09620312D

Patent No. 6569662

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Asundi, Vinod

APPLICANT: Zhang, Jie

APPLICANT: Ren, Feiyun

APPLICANT: Chen, Rui-hong

APPLICANT: Zhao, Qing A.

APPLICANT: Wehrman, Tom

APPLICANT: Xue, Aidong J.

APPLICANT: Yang, Yonghong

APPLICANT: Wang, Jian-Rui

APPLICANT: Zhou, Ping

APPLICANT: Ma, Yungqing

APPLICANT: Wang, Dunrui

APPLICANT: Wang, Zhiwei

APPLICANT: John Tillinghast

APPLICANT: Drmanac, Radoje T.

TITLE OF INVENTION: No. 6569662el Nucleic Acids and

FILE REFERENCE: 784CIP2B

CURRENT APPLICATION NUMBER: US/09/620,312D

CURRENT FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: 09/488,725

PRIOR FILING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 1105

SOFTWARE: pc-fl-genes Version 1.0

SEQ ID NO 625

LENGTH: 1878

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (945)..(1229)

US-09-620-312D-625

Query Match

Best Local Similarity: 91.8%; Pred. No. 9.6e-07;

Matches 45; Conservative 0; Mismatches 4; Indels 0;

Gaps 0;

DB

2 GCGTCGATCTTTTCTATGCCTCCCTGCGCGTGAATGGAGATACAG 50

464 GCGTCGATCTTTTCTATGCCTCCCTGCGCGTGAATGGAGATACAG 512

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RESULT 2
US-09-949-016-13185
; Sequence 13185, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13185
; LENGTH: 251769
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13185

Query Match          49.6%; Score 24.8; DB 4; Length 251769;
Best Local Similarity 72.7%; Pred. No. 31;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 7 ATCTTTTCATGCTCTCCCTGCTGGCGCTGATGGAGATACAG 50
Db 157799 ATCTGTTTATGTTTCTTCTGCTGCACTTGCTGGAGATTAG 157842

RESULT 3
US-09-949-016-13186
; Sequence 13186, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13186
; LENGTH: 251769
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13186

Query Match          49.6%; Score 24.8; DB 4; Length 251769;
Best Local Similarity 72.7%; Pred. No. 31;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 7 ATCTTTTCATGCTCTCCCTGCTGGCGCTGATGGAGATACAG 50
Db 157799 ATCTGTTTATGTTTCTTCTGCTGCACTTGCTGGAGATTAG 157842

RESULT 4
US-09-949-016-13187
; Sequence 13187, Application US/09949016
; Patent No. 6812339
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; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13187
; LENGTH: 266748
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13187

Query Match          49.6%; Score 24.8; DB 4; Length 266748;
Best Local Similarity 72.7%; Pred. No. 31;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 7 ATCTTTTCATGCTCTCCCTGCTGGCGCTGATGGAGATACAG 50
Db 157764 ATCTGTTTATGTTTCTTCTGCTGCACTTGCTGGAGATTAG 157807

RESULT 5
US-09-949-016-13188
; Sequence 13188, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13188
; LENGTH: 266748
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13188

Query Match          49.6%; Score 24.8; DB 4; Length 266748;
Best Local Similarity 72.7%; Pred. No. 31;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 7 ATCTTTTCATGCTCTCCCTGCTGGCGCTGATGGAGATACAG 50
Db 157764 ATCTGTTTATGTTTCTTCTGCTGCACTTGCTGGAGATTAG 157807

RESULT 6
US-09-949-016-16335
; Sequence 16335, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16335
LENGTH: 87190
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(87190)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16335

Query Match 48.4%; Score 24.2; DB 4; Length 87190;
Best Local Similarity 78.4%; Pred. No. 38;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 2 GGTGATCTTTTCTATGCTCTCCCTGCTGGGCTGA 38
Db 69962 GCTCATTTTCTTCTGCTACACGCTGTCACTGA 70018

RESULT 7
US-09-949-016-16782
Sequence 16782, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16782
LENGTH: 8044
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(8044)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16782

Query Match 47.6%; Score 23.8; DB 4; Length 8044;
Best Local Similarity 72.1%; Pred. No. 28;
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Oy 6 CATCTTTTCTATGCTCTCCCTGCTGGCTGATGGAGATC 48
Db 649 CTATGTACTACTACCCCTTCTGTGATGATGTGAGATGC 691

RESULT 8
US-09-103-840A-2
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.

APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 46.8%; Score 23.4; DB 3; Length 4403765;
Best Local Similarity 73.2%; Pred. No. 1,86+02;
Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 6 CATCTTTTCTATGCTCTCCCTGCTGGGCTGATGGAGAT 46
Db 551696 CACCGCTTGGTGTCTACTGATGTGCTGATGGATGAT 551736

RESULT 9
US-09-103-840A-1
Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 46.8%; Score 23.4; DB 3; Length 4411529;
Best Local Similarity 73.2%; Pred. No. 1,86+02;
Matches 30; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 6 CATCTTTTCTATGCTCTCCCTGCTGGGCTGATGGAGAT 46
Db 550253 CACCGCTTGGTGTCTACTGATGTGCTGATGGATGAT 550293

RESULT 10
US-09-064-703-8/c
Sequence 8, Application US/09064703
Patent No. 6033894
GENERAL INFORMATION:
APPLICANT: Craik, Charles S.
APPLICANT: Uhal, Ayce
APPLICANT: Ganem, Donald B.
TITLE OF INVENTION: Kaposi's Syndrome Herpesvirus
TITLE OF INVENTION: Protease and Assembly Protein Compositions and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 19

Query Match 45.6%; Score 22.8; DB 3; Length 1590;
Best Local Similarity 66.0%; Pred. No. 42;
Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CGCTGCATCTTTTCTATGCTCTCCCTGCGCGCTGATGAGATACAG 50
Db 1458 CGGTGCGCTGTGTGATGCTCTCGCTGCGAGCGGGGCTTCAG 1409

RESULT 13
US-09-064-703-5/c
Sequence 5, Application US/09064703
Patent No. 6033894

GENERAL INFORMATION:
APPLICANT: Craik, Charles S.
APPLICANT: Unal, Ayce
APPLICANT: Ganem, Donald E.
TITLE OF INVENTION: Kaposi's Syndrome Herpesvirus
TITLE OF INVENTION: Protease and Assembly Protein Compositions and
METHODS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,703
FILING DATE: 22-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/044,152
FILING DATE: 22-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Pettichory, Joanne R.
REGISTRATION NUMBER: P42,995
REFERENCE/DOCKET NUMBER: 2002-0002.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1605 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: KSHV Pr/AP polypeptide including SEQ ID NO:3
US-09-064-703-5

Query Match 45.6%; Score 22.8; DB 3; Length 1605;
Best Local Similarity 66.0%; Pred. No. 42;
Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CGCTGCATCTTTTCTATGCTCTCCCTGCGCGCTGATGAGATACAG 50
Db 1458 CGGTGCGCTGTGTGATGCTCTCGCTGCGAGCGGGGCTTCAG 1409

RESULT 14
US-09-064-703-4/c
Sequence 4, Application US/09064703
Patent No. 6033894
GENERAL INFORMATION:
APPLICANT: Craik, Charles S.
APPLICANT: Unal, Ayce

APPLICANT: Ganem, Donald E.
TITLE OF INVENTION: Kaposi's Syndrome Herpesvirus
TITLE OF INVENTION: Protease and Assembly Protein Compositions and
METHODS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,703
FILING DATE: 22-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/044,152
FILING DATE: 22-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Pettichory, Joanne R.
REGISTRATION NUMBER: P42,995
REFERENCE/DOCKET NUMBER: 2002-0002.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1701 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: KSHV Pr/AP polypeptide including SEQ ID NO:2
US-09-064-703-4

Query Match 45.6%; Score 22.8; DB 3; Length 1701;
Best Local Similarity 66.0%; Pred. No. 43;
Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CGCTGCATCTTTTCTATGCTCTCCCTGCGCGCTGATGAGATACAG 50
Db 1458 CGGTGCGCTGTGTGATGCTCTCGCTGCGAGCGGGGCTTCAG 1409

RESULT 15
US-08-770-379-17
Sequence 17, Application US/08770379
Patent No. 5849564
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelmann, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,379
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-770-379-17

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Query Match          45.6%; Score 22.8; DB 2; Length 35100;
Best Local Similarity 66.0%; Pred. No. 1e+02;
Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
1 CGCTGCATCTTTCTATGCTCTCCCTGCTGCGCGCTGATGCGAGATACAG 50
Db 30968 CGGTGCTGTGTGTGATGCTCTGCTGCTGAGGCGGCGGTGCTTCAAG 31017

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Search completed: February 9, 2005, 18:15:19
 Job time : 38.4494 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 17:59:05 ; Search time 98.5393 Seconds
(without alignments)
2920.530 Million cell updates/sec

Title: US-09-301-507-74_COPY_1_50
Perfect score: 50
Sequence: 1 CGCGCATCTTTTCTATGC.....GGCGCTATGGAGATACAG 50

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapept 1.0

Searched: 4313806 seqs, 287871033 residues
Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

1:	/cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2:	/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3:	/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4:	/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5:	/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6:	/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7:	/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8:	/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9:	/cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10:	/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11:	/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12:	/cgn2_6/ptodata/1/pubpna/US09 NEW_PUB.seq:*
13:	/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14:	/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15:	/cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16:	/cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17:	/cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18:	/cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19:	/cgn2_6/ptodata/1/pubpna/US10 NEW_PUB.seq:*
20:	/cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21:	/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	50	100.0	252	17	US-10-355-716-76	Sequence 76, Appl
2	50	100.0	336	17	US-10-355-716-74	Sequence 74, Appl
3	43.6	87.2	412	14	US-10-198-846-1775	Sequence 1775, Ap
4	42.6	85.2	455	14	US-10-198-846-8657	Sequence 8657, Ap
5	42.6	85.2	1878	15	US-10-037-270-625	Sequence 625, App
6	42.6	85.2	1878	17	US-10-117-722-625	Sequence 625, App
7	42.6	85.2	1894	18	US-10-723-860-6888	Sequence 6888, App
8	42.6	85.2	2061	14	US-10-198-846-11013	Sequence 11013, A
9	41	82.0	1872	18	US-10-723-860-2812	Sequence 2812, A
10	26.4	52.8	449	18	US-10-425-115-44104	Sequence 44104, A
11	24.4	48.8	535	13	US-10-027-632-270903	Sequence 270903,

12	24.4	48.8	535	13	US-10-027-632-270904	Sequence 270904,
13	24.4	48.8	535	17	US-10-027-632-270903	Sequence 270903,
14	24.4	48.8	530	17	US-10-027-632-270904	Sequence 270904,
15	24.4	48.8	540	13	US-10-027-632-276700	Sequence 276700,
16	24.4	48.8	540	17	US-10-027-632-276700	Sequence 276700,
17	24.4	48.8	871	17	US-10-424-599-109890	Sequence 109890,
18	24.4	48.8	3471	17	US-10-094-749-1170	Sequence 1170, Ap
19	23.8	47.6	215	16	US-10-437-963-44785	Sequence 44785, A
20	23.8	47.6	433	9	US-09-983-965-2915	Sequence 2915, Ap
21	23.4	46.8	886	18	US-10-767-701-11352	Sequence 11352, A
22	23.4	46.8	1521	17	US-10-282-122A-26603	Sequence 26603, A
23	23.4	46.8	1524	17	US-10-282-122A-28198	Sequence 28198, A
24	23.4	46.8	51657	17	US-10-057-475B-10475	Sequence 10475, A
25	23.4	46.8	51657	17	US-10-154-884B-10475	Sequence 10475, A
26	23.4	46.8	86114	15	US-10-080-170-648	Sequence 648, App
27	23.4	46.8	86114	18	US-10-080-170-648	Sequence 648, App
28	23.4	46.8	86114	18	US-10-468-356-648	Sequence 648, App
29	23.4	46.8	275449	13	US-10-087-192-520	Sequence 520, App
30	23.4	46.8	317876	18	US-10-741-601-5629	Sequence 5629, Ap
31	23.2	46.4	707	17	US-10-424-589-85536	Sequence 85536, A
32	23.2	46.4	2620	18	US-10-437-963-91254	Sequence 91254, A
33	23	46.0	284	18	US-10-437-963-7487	Sequence 7487, A
34	23	46.0	650	18	US-10-437-963-35252	Sequence 35252, A
35	23	46.0	684973	9	US-09-263-959-1	Sequence 1, Appl1
36	22.8	45.6	1521	17	US-10-282-122A-25599	Sequence 25599, A
37	22.6	45.2	1094	17	US-10-424-599-63356	Sequence 63356, A
38	22.6	45.2	21565	17	US-10-052-482-61	Sequence 61, Appl
39	22.6	45.2	296405	13	US-10-087-192-1036	Sequence 1036, Appl
40	22.6	45.2	302603	17	US-10-271-416-8	Sequence 8, Appl1
41	22.6	45.2	606398	18	US-10-719-993-6782	Sequence 6782, Appl
42	22.6	45.2	1980090	18	US-10-719-993-6815	Sequence 6815, App
43	22.4	44.8	598	13	US-10-027-632-194004	Sequence 194004,
44	22.4	44.8	598	13	US-10-027-632-194005	Sequence 194005,
45	22.4	44.8	598	17	US-10-027-632-194904	Sequence 194904,

ALIGNMENTS

RESULT 1
US-10-355-716-76
; Sequence 76, Application US/10355716
; Publication No. US20030216339A1

GENERAL INFORMATION:
APPLICANT: Cynader, Max
Prasad, Shiv

TITLE OF INVENTION: GENE SEQUENCES ASSOCIATED WITH NEURAL PLASTICITY AND METHODS RELATED THERETO

NUMBER OF SEQUENCES: 132

CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentm Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/355, 716
FILING DATE: 31-Jan-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/301,507
FILING DATE: 28-Apr-1999

ATTORNEY/AGENT INFORMATION:
NAME: Potler, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 230018, 401C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-10-355-716-76
SEQUENCE DESCRIPTION: SEQ ID NO: 76:
Query Match 100.0%; Score 50; DB 17; Length 252;
Best Local Similarity 100.0%; Pred. No. 6,9e-10;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGCTGCATCTTTTCTATGCTCTCCCTGCGCGCTGATGGAGATACAG 50
Db 1 CGCTGCATCTTTTCTATGCTCTCCCTGCGCGCTGATGGAGATACAG 50

RESULT 2
US-10-355-716-74
Sequence 74, Application US/10355716
Publication No. US20030216339A1
GENERAL INFORMATION:
APPLICANT: Cynader, Max
Praised, Shiv
TITLE OF INVENTION: GENE SEQUENCES ASSOCIATED WITH NEURAL PLASTICITY AND METHODS RELATED THERETO
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/355,716
FILING DATE: 31-Jan-2003
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/301,507
FILING DATE: 28-Apr-1999
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 230018.401C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-10-355-716-74
SEQUENCE DESCRIPTION: SEQ ID NO: 74:
Query Match 100.0%; Score 50; DB 17; Length 336;
Best Local Similarity 100.0%; Pred. No. 6,9e-10;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGCTGCATCTTTTCTATGCTCTCCCTGCGCGCTGATGGAGATACAG 50
Db 1 CGCTGCATCTTTTCTATGCTCTCCCTGCGCGCTGATGGAGATACAG 50

RESULT 3
US-10-198-846-1775
Sequence 1775, Application US/10198846
Publication No. US2003009974A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1775
LENGTH: 412
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 3, 203, 293, 343, 398
OTHER INFORMATION: n = A,T,C or G
US-10-198-846-1775

Query Match 87.2%; Score 43.6; DB 14; Length 412;
Best Local Similarity 92.0%; Pred. No. 2,5e-07;
Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGCTGCATCTTTTCTATGCTCTCCCTGCGCGCTGATGGAGATACAG 50
Db 49 CGCTGCATCTTTTCTATGCTCTCCCTGCGCGCTGATGGAGATACAG 98

RESULT 4
US-10-198-846-8657
Sequence 8657, Application US/10198846
Publication No. US2003009974A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8657
LENGTH: 455
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 2, 7, 404, 454
OTHER INFORMATION: n = A,T,C or G
US-10-198-846-8657

Query Match 85.2%; Score 42.6; DB 14; Length 455;
Best Local Similarity 91.8%; Pred. No. 6,4e-07;
Matches 45; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GCTGCATCTTTTCTATGCTCTCCCTGCGCGCTGATGGAGATACAG 50

Db 60 GCTGCATCTTTTCTATGCTCTCCCTGCTGGATGAATGAGGAGATACAG 108

RESULT 5

US-10-037-270-625

; Sequence 625, Application US/10037270
; Publication No. US20030104529A1

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

; APPLICANT: Zhang, Jie

; APPLICANT: Ren, Feiyan

; APPLICANT: Chen, Rui-hong

; APPLICANT: Zhao, Qing A.

; APPLICANT: Wehrman, Tom

; APPLICANT: Xue, Aidong J.

; APPLICANT: Yang, Yonghong

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Zhou, Ping

; APPLICANT: Ma, Yuning

; APPLICANT: Wang, Dunrui

; APPLICANT: Wang, Zhiwei

; APPLICANT: Tillinghaet, John

; APPLICANT: Drmanac, Radoje T.

; TITLE OF INVENTION: No. US20030104529A1e1 Nucleic Acids and

; FILE REFERENCE: 784CIP2B

; CURRENT APPLICATION NUMBER: US/10/037,270

; PRIOR FILING DATE: 2002-01-04

; PRIOR APPLICATION NUMBER: 09/552,317

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: 09/488,725

; PRIOR FILING DATE: 2000-01-21

; NUMBER OF SEQ ID NOS: 1104

; SOFTWARE: pc_Fl_genes Version 1.0

; SEQ ID NO 625

; LENGTH: 1878

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (945)..(1229)

US-10-037-270-625

Query Match

Best Local Similarity 91.8%; Score 42.6; DB 15; Length 1878;
Matches 45; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 464 GCTGCATCTTTTCTATGCTCTCCCTGCTGGATGAATGAGGAGATACAG 512

RESULT 6

US-10-117-722-625

; Sequence 625, Application US/10117722
; Publication No. US20030219744A1

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

; APPLICANT: Zhang, Jie

; APPLICANT: Drmanac, Radoje T.

; TITLE OF INVENTION: No. US20030219744A1e1 Nucleic Acids and

; FILE REFERENCE: 784CIP2B

; CURRENT APPLICATION NUMBER: US/10/117,722

; PRIOR FILING DATE: 2002-04-04

; PRIOR APPLICATION NUMBER: 09/620,312

; PRIOR FILING DATE: 2000-07-19

; PRIOR APPLICATION NUMBER: 09/552,317

; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pc_Fl_genes Version 1.0
; SEQ ID NO 625
; LENGTH: 1878
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: CDS

; LOCATION: (945)..(1229)

US-10-117-722-625

Query Match

Best Local Similarity 91.8%; Score 42.6; DB 17; Length 1878;
Matches 45; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 464 GCTGCATCTTTTCTATGCTCTCCCTGCTGGATGAATGAGGAGATACAG 512

RESULT 7

US-10-723-860-6888

; Sequence 6888, Application US/10723860
; Publication No. US20040253606A1

; GENERAL INFORMATION:

; APPLICANT: Aziz, Natsasha

; APPLICANT: Giesburg, Wendy M.

; APPLICANT: Zlocnik, Albert

; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &

; FILE REFERENCE: 05882.0193.NFUS01

; CURRENT APPLICATION NUMBER: US/10/723,860

; PRIOR FILING DATE: 2003-11-26

; PRIOR APPLICATION NUMBER: 60/429,739

; PRIOR FILING DATE: 2002-11-26

; NUMBER OF SEQ ID NOS: 8393

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 6888

; LENGTH: 1894

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (650)..(669)

; OTHER INFORMATION: n is a, c, g, or t

US-10-723-860-6888

Query Match

Best Local Similarity 91.8%; Score 42.6; DB 18; Length 1894;
Matches 45; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 435 GCTGCATCTTTTCTATGCTCTCCCTGCTGGATGAATGAGGAGATACAG 483

RESULT 8

US-10-198-846-11013

; Sequence 11013, Application US/10198846
; Publication No. US20030099974A1

; GENERAL INFORMATION:

; APPLICANT: Li, Jie, James

; APPLICANT: Xu, Yongyao

; APPLICANT: Wang, Youzhen

; APPLICANT: Steinmann, Kathleen

; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS

; FILE REFERENCE: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

; CURRENT APPLICATION NUMBER: US/10/198,846

; PRIOR FILING DATE: 2000-07-19

; PRIOR APPLICATION NUMBER: 09/552,317

; PRIOR FILING DATE: 2000-07-19

; PRIOR APPLICATION NUMBER: 09/552,317

; PRIOR FILING DATE: 2000-07-19

; PRIOR APPLICATION NUMBER: 09/552,317

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; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11013
; LENGTH: 2061
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 2, 3, 1831, 1832, 1833, 1834, 1835, 1836, 1837, 1838,
; LOCATION: 1839, 1840, 1841, 1842, 1843, 1844, 1845, 1846, 1847, 1848,
; LOCATION: 1849, 1850, 1851, 1852, 1853, 1854, 1855, 1856, 1860, 2009,
; LOCATION: 2033, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057,
; LOCATION: 2058, 2059, 2060, 2061
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-11013

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Query Match      85.2%; Score 42.6; DB 14; Length 2061;
Best Local Similarity 91.8%; Pred. No. 8.2e-07;
Matches 45; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY      2 GCTGCATCTTTTCTATGCTCTCCCTGCTGCGCTGATGGAGATACAG 50
Db      427 GCTGCATCTTTTCTATGCTCTCCCTGCTGCTGATGATGAGATACAG 475

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RESULT 9
US-10-723-860-2812
; Sequence 2812, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natascha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnick, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2812
; LENGTH: 1872
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2812

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Query Match      82.0%; Score 41; DB 18; Length 1872;
Best Local Similarity 89.8%; Pred. No. 3.5e-06;
Matches 44; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY      2 GCTGCATCTTTTCTATGCTCTCCCTGCTGCGCTGATGGAGATACAG 50
Db      435 GCTGCATCTTTTCTATGCTCTCCCTGCTGCTGATGAGGAGATACAG 483

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RESULT 10
US-10-425-115-44104
; Sequence 44104, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: la Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

```

```

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 44104
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_140229C.1
US-10-425-115-44104

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Query Match      52.8%; Score 26.4; DB 18; Length 449;
Best Local Similarity 83.3%; Pred. No. 1.8;
Matches 30; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY      9 CTTTCTATGCTCTCCCTGCTGCGCTGATGGAG 44
Db      131 CTTTCTATGCTCTGCTGCTGAGCGCTGCAGAG 166

```

```

RESULT 11
US-10-027-632-270903
; Sequence 270903, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 270903
; LENGTH: 535
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-270903

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```

Query Match      48.8%; Score 24.4; DB 13; Length 535;
Best Local Similarity 73.8%; Pred. No. 12;
Matches 31; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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QY      6 CATCTTTTCTATGCTCTCCCTGCTGCGCTGATGGAGATATA 47
Db      224 CTTTGTACTACTACACCTTCTGCTGATGATGAGATATA 265

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```

RESULT 12
US-10-027-632-270904
; Sequence 270904, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: Polymorphisms in the Human Genome

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Query Match	48.8%	Score 24.4	DB 17	Length 535
Best Local Similarity	73.8%	Mid. No. 12		
Matches 31	Conservative 0	Mismatches 11	Indels 0	Gaps 0
QY	6	CATCTTTTCATGCTCCCTGCGGGCGGCGAGGAGATA	47	

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RESULT 15
US-10-027-632-276700/c
; Sequence 276700, Application US/10027632
; Publication No. US2002019837A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.19
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 276700

```

; LENGTH: 540
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-276700

Query Match 48.8%; Score 24.4; DB 13; Length 540;
Best Local Similarity 73.8%; Pred. No. 12;
Matches 31; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 6 CATCTTTTCTAGCCTCTCCCTGCTGCGCTGATGGAGATA 47
Db 312 CTTTGTCTACTAATCTACCCCTTCTCTGATGATGAGATA 271

Search completed: February 9, 2005, 20:39:51
Job time : 101.539 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 15:18:20 ; Search time 54.809 Seconds
(without alignments)
2686.875 Million cell updates/sec

Title: US-09-301-507-74_COPY_1_90

Perfect score: 90

Sequence: 1 CGCTGATCTTTTCTATGC.....TNTATGATCGACTCGAC 90

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfilee1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64.2	71.3	1878	4	US-09-620-312D-625
2	27.6	30.7	449	4	US-09-621-976-14464
3	26.8	29.8	684	4	US-09-489-039A-4463
4	26.8	29.8	1362	4	US-09-711-164-178
5	26.8	29.8	1386	4	US-09-489-039A-4437
6	26.8	29.8	1560	4	US-09-489-039A-4420
7	26.8	29.8	4403765	3	US-09-103-840A-2
8	26.8	29.8	4411529	3	US-09-103-840A-1
9	26.6	29.6	601	4	US-09-949-016-50118
10	26.4	29.3	9069	4	US-09-949-016-15856
11	26.2	29.1	105733	4	US-09-949-016-15880
12	26	28.9	2200	2	US-08-819-825-1
13	26	28.9	2200	3	US-09-163-642-1
14	25.8	28.7	15379	4	US-09-949-016-14191
15	25.8	28.7	20634	4	US-09-949-016-16227
16	25.8	28.7	76563	4	US-09-949-016-17099
17	25.8	28.7	78469	4	US-09-949-016-12497
18	25.8	28.7	132438	4	US-09-949-016-14349
19	25.8	28.7	132438	4	US-09-949-016-14350
20	25.8	28.7	151089	4	US-09-949-016-14348
21	25.8	28.7	524032	4	US-09-949-016-16928
22	25.8	28.7	524032	4	US-09-949-016-16929
23	25.8	28.7	524032	4	US-09-949-016-16930
24	25.8	28.7	524032	4	US-09-949-016-16931
25	25.8	28.7	529885	4	US-09-949-016-14340
26	25.8	28.7	529885	4	US-09-949-016-14341
27	25.8	28.7	529885	4	US-09-949-016-14342

ALIGNMENTS

28	25.8	28.7	529885	4	US-09-949-016-14343	Sequence 14343, A
29	25.8	28.7	529885	4	US-09-949-016-14344	Sequence 14344, A
30	25.8	28.7	529885	4	US-09-949-016-14345	Sequence 14345, A
31	25.8	28.7	529885	4	US-09-949-016-14346	Sequence 14346, A
32	25.8	28.7	529885	4	US-09-949-016-14347	Sequence 14347, A
33	25.6	28.4	18112	4	US-09-949-016-13648	Sequence 13648, A
34	25.4	28.2	601	4	US-09-949-016-50119	Sequence 50119, A
35	25.4	28.2	97989	4	US-09-949-016-13208	Sequence 13208, A
36	25.4	28.2	134140	4	US-09-949-016-12672	Sequence 12672, A
37	25.4	28.2	134241	4	US-09-949-016-12424	Sequence 12424, A
38	25.4	28.2	134242	4	US-09-949-016-15813	Sequence 15813, A
39	25.4	28.2	134242	4	US-09-949-016-15814	Sequence 15814, A
40	25.4	28.2	134242	4	US-09-949-016-15815	Sequence 15815, A
41	25.2	28.0	86380	4	US-09-949-016-14837	Sequence 14837, A
42	25.2	28.0	92155	4	US-09-949-016-17484	Sequence 17484, A
43	25.2	28.0	163022	4	US-09-949-016-16515	Sequence 16515, A
44	24.8	27.6	601	4	US-09-949-016-185803	Sequence 185803, A
45	24.8	27.6	601	4	US-09-949-016-185804	Sequence 185804, A

RESULT 1
US-09-620-312D-625
; Sequence 625, Application US/09620312D
; Patent No. 6569662

GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyun
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundong
; APPLICANT: Wang, Duntui
; APPLICANT: Wang, Zhwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc FL_genes Version 1.0
; SEQ ID NO 625
; LENGTH: 1878
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (945)..(1229)
; US-09-620-312D-625

Query Match 71.3%; Score 64.2; DB 4; Length 1878;
Best Local Similarity 89.9%; Pred. No. 8.8e-15;
Matches 80; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

2 GCTGATCTTTTCTATGCTCTCCCTGCTGCGCTGATGAGATACAGACAGCAAAACG 61
464 GCTGATCTTTTCTATGCTCTCCCTGCTGCGCTGATGAGATACAGACAGCAAAACG 523

QY 62 GACAGCTGTTGATGATGACTCGGACC 90
DB 524 GACAGCTGAT-TGATATGAGCTCGACC 551

RESULT 2

US-09-621-976-14464
; Sequence 14464, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J. B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J. Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 14464
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-14464

Query Match 30.7%; Score 27.6; DB 4; Length 449;
Best Local Similarity 62.7%; Pred. No. 0.92; Mismatches 25; Indels 0; Gaps 0;
Matches 42; Conservative 0;

QY 23 TCCCTGCTGCGCTGATGGAGATACAGACGAAAGCAGCTGTCATGATGCA 82
DB 243 TCCCTGCTGATCAGTGAGGGGTCACAGACGCTGACAGCTGATGCA 302

QY 83 CTGGAC 89
DB 303 GACGGTC 309

RESULT 3

US-09-489-039A-4463/c
; Sequence 4463, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 4463
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-4463

Query Match 29.8%; Score 26.8; DB 4; Length 684;
Best Local Similarity 68.5%; Pred. No. 2.2; Mismatches 17; Indels 0; Gaps 0;
Matches 37; Conservative 0;

QY 17 ATGCTCTCCCTGCTGCGCTGATGGAGATACAGACGAAACGAGCAGCTCG 70
DB 473 ATGGGCGAGCTGCTGCTGCTGATGGAAGATATCGAGCAAGGTTGACCGCGG 420

RESULT 4

US-09-711-164-178
; Sequence 178, Application US/09711164
; Patent No. 6589738
; GENERAL INFORMATION:
; APPLICANT: Foreysch, R. Allyn

APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERET
; FILE REFERENCE: ELITRA.008A
; CURRENT APPLICATION NUMBER: US/09/711,164
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/164415
; PRIOR FILING DATE: 1999-11-9
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1362)
US-09-711-164-178

Query Match 29.8%; Score 26.8; DB 4; Length 1362;
Best Local Similarity 68.5%; Pred. No. 3; Mismatches 17; Indels 0; Gaps 0;
Matches 37; Conservative 0;

QY 17 ATGCTCTCCCTGCTGCGCTGATGGAGATACAGACGAAACGAGCAGCTCG 70
DB 889 ATGGGCGAGCTACTGTGCTGATGCAAGATATCGAAGCAAGCTGACCGCGG 942

RESULT 5

US-09-489-039A-4437/c
; Sequence 4437, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 4437
; LENGTH: 1386
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-4437

Query Match 29.8%; Score 26.8; DB 4; Length 1386;
Best Local Similarity 68.5%; Pred. No. 3; Mismatches 17; Indels 0; Gaps 0;
Matches 37; Conservative 0;

QY 17 ATGCTCTCCCTGCTGCGCTGATGGAGATACAGACGAAACGAGCAGCTCG 70
DB 510 ATGGGCGAGCTGCTGCTGATGGAAGATATCGAAGCAAGGTTGACCGCGG 457

RESULT 6

US-09-489-039A-4420
; Sequence 4420, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 4420
; LENGTH: 1560

TYPE: DNA
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-4420

Query Match
Best Local Similarity 29.8%; Score 26.8; DB 4; Length 1560;
Matches 37; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 17 ATGCTCTCCCTGCTGCGCTGATGGAGATACAGACGAAACGACAGCTCG 70
Db 1084 ATGGCGACGCTGCTGCTGATGTAAGATATCGAGACGAGTTGACCGCGC 1137

RESULT 7
US-09-103-840A-2
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: "a" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match
Best Local Similarity 29.8%; Score 26.8; DB 3; Length 4403765;
Matches 37; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 29 CTGGCGCTGATGGAGATACAGACGAAACGACAGCTCGTTCATGATGAC 83
Db 781400 CCGACGCCCTGGCGGATACAGACCGAACCGAGAGAGACGATGATGACGAC 781454

RESULT 8
US-09-103-840A-1
Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match
Best Local Similarity 29.8%; Score 26.8; DB 3; Length 4411529;
Matches 67.3%; Pred. No. 78;

Matches 37; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 29 CTGGCGCTGATGGAGATACAGACGAAACGACAGCTCGTTCATGATGAC 83
Db 779439 CCGACGCCCTGGCGGATACAGACCGAACCGAGAGAGACGATGATGACGAC 779493

RESULT 9
US-09-949-016-50118
Sequence 50118, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CLO01307
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 50118
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-50118

Query Match
Best Local Similarity 29.6%; Score 26.6; DB 4; Length 601;
Matches 35; Conservative 1; Mismatches 15; Indels 0; Gaps 0;

Qy 15 CTATGCTCTCCCTGCTGCGCTGATGGAGATACAGACGAAACGAC 65
Db 296 CTAGAGGCTCTCATCTGCGGATGATGGAGATGATGACATCATCGGACA 346

RESULT 10
US-09-949-016-15856
Sequence 15856, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CLO01307
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15856
LENGTH: 9069
TYPE: DNA
ORGANISM: Human
US-09-949-016-15856

Query Match
Best Local Similarity 29.3%; Score 26.4; DB 4; Length 9069;
Matches 45; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 14 TCTATGCTCTCCCTGCTGCGCTGATGGAGATACAGACGAAACGACAGCTCGTNT 73
Db 4110 TCTAGCTCTCCCTATGATGAGATATGGAGAACGACGATACAGAGATTCTAAGTCT 4169

QY 74 CAGATGACTCGGACC 90
Db 4170 CAGGTCTCCAGGCC 4186

RESULT 11

US-09-949-016-13080/c
Sequence 13080, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTNER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13080
LENGTH: 105733
TYPE: DNA
ORGANISM: Human
US-09-949-016-13080

Query Match 29.1%; Score 26.2; DB 4; Length 105733;
Best Local Similarity 67.3%; Pred. No. 32;
Matches 37; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 11 TTTTCTATGCTCTCCCTGCTGCGCGCTGATGGAGATACAGACGCAAAACGGACA 65
Db 92409 TGTCTATCTTAACCTTTCGTGAGTGAAGGATGATGACAGAGAAAGACACA 92355

RESULT 12

US-08-819-825-1/c
Sequence 1, Application US/08819825
Patent No. 5866118
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58661180 No. 5866118disk of No. 5866118th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,825
FILING DATE: 18-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4758.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123

TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-819-825-1

Query Match 28.9%; Score 26; DB 2; Length 2200;
Best Local Similarity 58.7%; Pred. No. 7.5;
Matches 44; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 3 CTGCATCTTTTCTATGCTCTCCCTGCTGCGCGCTGATGGAGATACAGACGCAAAACGG 62
Db 2013 CTGGCCCTTTTGGATCAATTTCCCTTCGCGAGTGAATGATCTAAACATCAATTCGG 1954

QY 63 ACAGCTGNTTCATG 77
Db 1953 AATCATGGGTTATG 1939

RESULT 13

US-09-163-642-1/c
Sequence 1, Application US/09163642
Patent No. 6221644
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 62216440 No. 6221644disk of No. 6221644th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/163,642
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/819,825
FILING DATE: 18-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4758.200-US
TELECOMMUNICATION INFORMATION:
TELEFAX: 212 867 0123
TELEPHONE: 212 867 0298
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-163-642-1

Query Match 28.9%; Score 26; DB 3; Length 2200;
Best Local Similarity 58.7%; Pred. No. 7.5;
Matches 44; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 3 CTGCATCTTTTCTATGCTCTCCCTGCTGCGCGCTGATGGAGATACAGACGCAAAACGG 62
||| ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||

Db 2013 CTGGCGCTTTTGATCATTCCTTCGCGAGTATGTATCTAAACATCAATTCGG 1954
 QY 63 ACAGCTCGTTCATG 77
 Db 1953 AATCATGGGCTATG 1939

RESULT 14

US-09-949-016-14191
 ; Sequence 14191, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14191
 ; LENGTH: 15379
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-949-016-14191

Query Match 28.7%; Score 25.8; DB 4; Length 15379;
 Best Local Similarity 55.8%; Pred. No. 20;
 Matches 48; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 3 CTGCATCTTTTCTATGCTCTCCCTGCGGCTGATGGAGATACAGACGCAAAACGG 62
 Db 3888 CTGCATCTTTTCTATGCTCTCCCTGCGGCTGATGGAGATACAGACGCAAAACCT 3947
 QY 63 ACAGCTCGTTCATGACTCGGA 88
 Db 3948 ATGGTTGAGAAATAGTACCTAGGA 3973

RESULT 15

US-09-949-016-16627
 ; Sequence 16627, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 16627
 ; LENGTH: 20634
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-949-016-16627

Query Match 28.7%; Score 25.8; DB 4; Length 20634;
 Best Local Similarity 55.8%; Pred. No. 23;
 Matches 48; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 3 CTGCATCTTTTCTATGCTCTCCCTGCGGCTGATGGAGATACAGACGCAAAACGG 62
 Db 3888 CTGCATCTTTTCTATGCTCTCCCTGCGGCTGATGGAGATACAGACGCAAAACCT 3953
 QY 63 ACAGCTCGTTCATGACTCGGA 88
 Db 3954 ATGGTTGAGAAATAGTACCTAGGA 3979

Search completed: February 9, 2005, 18:15:27
 Job time : 62.809 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 17:59:05 ; Search time 177.371 Seconds
(without alignments)
2920.530 Million cell updates/sec

Title: US-09-301-507-74_COPY_1_90

Sequence: 1 CGCGCATCTTTTCTATGC.....TNTCATGATGACTCGAAC 90

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 413806 seqs, 287871033 residues

Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/FCR_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09C_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	89	98.9	336	17	US-10-355-716-74
2	86	95.6	252	17	US-10-355-716-76
3	65.2	72.4	412	14	US-10-198-846-1775
4	64.2	71.3	455	14	US-10-198-846-8657
5	64.2	71.3	1878	15	US-10-037-270-625
6	64.2	71.3	1878	17	US-10-117-722-625
7	64.2	71.3	1894	18	US-10-723-860-6888
8	64.2	71.3	2061	14	US-10-198-846-11013
9	62.6	69.6	1872	18	US-10-723-860-2812
10	31	34.4	465	10	US-09-918-995-15342
11	28.2	31.3	449	18	US-10-425-115-44104

12	27.8	30.9	1362	17	US-10-282-122A-42325	Sequence 42325, A
13	27.4	30.4	247461	18	US-10-322-281-131	Sequence 131, App
14	27	30.0	294	9	US-09-294-093B-3147	Sequence 3147, Ap
15	27	30.0	745	13	US-10-027-632-161738	Sequence 161738, A
16	27	30.0	745	17	US-10-027-632-161738	Sequence 161738, A
17	27	30.0	793	13	US-10-027-632-164644	Sequence 164644, A
18	27	30.0	793	17	US-10-027-632-164644	Sequence 164644, A
19	26.8	29.8	1120	17	US-10-282-122A-19217	Sequence 19217, A
20	26.8	29.8	1128	17	US-10-282-122A-23264	Sequence 23264, A
21	26.8	29.8	1362	9	US-09-815-242-6166	Sequence 6166, Ap
22	26.8	29.8	1362	16	US-10-287-274-178	Sequence 178, App
23	26.8	29.8	1362	17	US-10-282-122A-6414	Sequence 6414, Ap
24	26.4	29.3	2215	18	US-10-741-601-239	Sequence 239, App
25	26.4	29.3	17150	18	US-10-741-601-5688	Sequence 5688, App
26	26.2	29.1	2163	17	US-10-425-114-32715	Sequence 32715, A
27	26.2	29.1	2163	18	US-10-425-115-66386	Sequence 66386, A
28	26	28.9	1829	17	US-10-108-260A-1668	Sequence 1668, Ap
29	25.8	28.7	219	18	US-10-437-963-7315	Sequence 7315, Ap
30	25.8	28.7	377	18	US-10-425-115-1423	Sequence 1423, Ap
31	25.8	28.7	711	18	US-10-767-701-11796	Sequence 11796, A
32	25.8	28.7	785	9	US-09-823-245A-18	Sequence 18, Appl
33	25.8	28.7	92563	11	US-09-997-722-70	Sequence 70, Appl
34	25.8	28.7	275449	13	US-10-087-192-520	Sequence 520, App
35	25.8	28.7	317876	18	US-10-741-601-5629	Sequence 5629, Ap
36	25.6	28.4	489	18	US-10-425-115-179016	Sequence 179016, A
37	25.6	28.4	609	14	US-10-198-846-9509	Sequence 9509, Ap
38	25.6	28.4	684973	9	US-09-263-959-1	Sequence 1, Appl
39	25.4	28.2	2182	17	US-10-425-114-30015	Sequence 30015, A
40	25.4	28.2	2497	17	US-10-424-599-97141	Sequence 97141, A
41	25.4	28.2	13784	18	US-10-719-993-6793	Sequence 6793, Ap
42	25.4	28.2	15922	18	US-10-741-601-5643	Sequence 5643, Ap
43	25.4	28.2	15922	18	US-10-719-993-6795	Sequence 6795, Ap
44	25.4	28.2	23909	13	US-10-087-192-604	Sequence 604, App
45	25.4	28.2	28553	18	US-10-741-601-5763	Sequence 5763, Ap

ALIGNMENTS

RESULT 1
US-10-355-716-74
Sequence 74, Application US/10355716
Publication No. US20030216339A1
GENERAL INFORMATION:
APPLICANT: Cynader, Max
TITLE OF INVENTION: GENE SEQUENCES ASSOCIATED WITH NEURAL PLASTICITY AND METHODS RELATED THERETO
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/355, 716
FILING DATE: 31-Jan-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/301,507
FILING DATE: 28-Apr-1999
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 230018.401C1
TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-10-355-716-74

Query Match 98.9%; Score 89; DB 17; Length 336;
Best Local Similarity 100.0%; Pred. No. 7, 2e-25;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCTGATCTTTTCTATGCTCTCCCTGCGCGCTGATGGAGATACAGACGAAAC 60
DB 1 CGCTGATCTTTTCTATGCTCTCCCTGCGCGCTGATGGAGATACAGACGAAAC 60
QY 61 GGACAGCTCGTNTCATGATGACTCGGACC 90
DB 61 GGACAGCTCGTNTCATGATGACTCGGACC 90

RESULT 2

US-10-355-716-76
Sequence 76, Application US/10355716
Publication No. US20030216339A1

GENERAL INFORMATION:

APPLICANT: Cynader, Max
Prasad, Shiv

TITLE OF INVENTION: GENE SEQUENCES ASSOCIATED WITH NEURAL
PLASTICITY AND METHODS RELATED THEREO

NUMBER OF SEQUENCES: 132

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/355,716

FILING DATE: 31-Jan-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/301,507

FILING DATE: 28-Apr-1999

ATTORNEY/AGENT INFORMATION:

NAME: Potter, Jane E. R.

REGISTRATION NUMBER: 33,332

REFERENCE/DOCKET NUMBER: 230018, 401C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 76:

SEQUENCE CHARACTERISTICS:

LENGTH: 252 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 76:
US-10-355-716-76

Query Match 95.6%; Score 86; DB 17; Length 252;
Best Local Similarity 98.9%; Pred. No. 1e-23;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCTGATCTTTTCTATGCTCTCCCTGCGCGCTGATGGAGATACAGACGAAAC 60
DB 1 CGCTGATCTTTTCTATGCTCTCCCTGCGCGCTGATGGAGATACAGACGAAAC 60
QY 61 GGACAGCTCGTNTCATGATGACTCGG 87
DB 61 GGACAGCTCGTNTCATGATGACTCGG 87

RESULT 3

US-10-198-846-1775
Sequence 1775, Application US/10198846
Publication No. US2003009974A1

GENERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: Xu, Yongyao

APPLICANT: Wang, Youzhen

APPLICANT: Steinmann, Kathleen

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS

TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

TITLE OF INVENTION: THERAPY OF BREAST CANCER

FILE REFERENCE: MEI-049

CURRENT APPLICATION NUMBER: US/10/198,846

CURRENT FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/306,220

PRIOR FILING DATE: 2001-07-18

NUMBER OF SEQ ID NOS: 14084

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1775

LENGTH: 412

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc.feature

LOCATION: 3, 203, 293, 343, 398

OTHER INFORMATION: n = A,T,C or G

US-10-198-846-1775

Query Match 72.4%; Score 65.2; DB 14; Length 412;
Best Local Similarity 90.0%; Pred. No. 2, 1e-15;
Matches 81; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 CGCTGATCTTTTCTATGCTCTCCCTGCGCGCTGATGGAGATACAGACGAAAC 60
DB 49 CGCTGATCTTTTCTATGCTCTCCCTGCGCGCTGATGGAGATACAGACGAAAC 108

QY 61 GGACAGCTCGTNTCATGATGACTCGGACC 90

DB 109 GGACAGCTCAT-TCATATGACTCGGACC 137

RESULT 4

US-10-198-846-8657
Sequence 8657, Application US/10198846
Publication No. US2003009974A1

GENERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: Xu, Yongyao

APPLICANT: Wang, Youzhen

APPLICANT: Steinmann, Kathleen

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS

TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

TITLE OF INVENTION: THERAPY OF BREAST CANCER

FILE REFERENCE: MEI-049

CURRENT APPLICATION NUMBER: US/10/198,846

CURRENT FILING DATE: 2002-07-18

PRIOR APPLICATION NUMBER: 60/306,220

PRIOR FILING DATE: 2001-07-18

NUMBER OF SEQ ID NOS: 14084

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 8657

LENGTH: 455

TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2, 7, 404, 454
OTHER INFORMATION: n = A,T,C or G
US-10-198-846-8657

Query Match 71.3%; Score 64.2; DB 14; Length 455;
Best Local Similarity 89.9%; Pred. No. 5.3e-15;
Matches 80; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 2 GGTGATCTTTTTCATGCTCTCCCTGCTGGCGCTGATGGAGATACAGACAGCAAAACG 61
Db 60 GGTGATCTTTTTCATGCTCTCCCTGCTGGCGATATAGGAGATACAGACAGTAAACG 119

Qy 62 GACAGCTGTTTCATGATGATGACTCGGACC 90
Db 120 GACAGCTCAT-TCATTAATGAGACTCGGACC 147

RESULT 5
US-10-037-270-625
Sequence 625, Application US/10037270
Publication No. US20030104529A1

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Weinman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundong
APPLICANT: Wang, Duntui
APPLICANT: Wang, Zhimei
APPLICANT: Tillinghaert, John
APPLICANT: Drmanac, Radote T.
TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/10/037,270
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: pc_fl_genes Version 1.0
SEQ ID NO 625
LENGTH: 1878
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (945) .. (1229)
US-10-037-270-625

Query Match 71.3%; Score 64.2; DB 15; Length 1878;
Best Local Similarity 89.9%; Pred. No. 7.6e-15;
Matches 80; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 2 GGTGATCTTTTTCATGCTCTCCCTGCTGGCGCTGATGGAGATACAGACAGCAAAACG 61
Db 464 GGTGATCTTTTTCATGCTCTCCCTGCTGGGATATAGGAGATACAGACAGTAAACG 523

Qy 62 GACAGCTGTTTCATGATGATGACTCGGACC 90
Db 524 GACAGCTCAT-TCATTAATGAGACTCGGACC 551

RESULT 6
US-10-117-722-625
Sequence 625, Application US/10117722
Publication No. US20030219744A1

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Drmanac, Radote T.
TITLE OF INVENTION: No. US20030219744A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2Bclp
CURRENT APPLICATION NUMBER: US/10/117,722
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: pc_fl_genes Version 1.0
SEQ ID NO 625
LENGTH: 1878
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (945) .. (1229)
US-10-117-722-625

Query Match 71.3%; Score 64.2; DB 17; Length 1878;
Best Local Similarity 89.9%; Pred. No. 7.6e-15;
Matches 80; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 2 GGTGATCTTTTTCATGCTCTCCCTGCTGGCGCTGATGGAGATACAGACAGCAAAACG 61
Db 464 GGTGATCTTTTTCATGCTCTCCCTGCTGGGATATAGGAGATACAGACAGTAAACG 523

Qy 62 GACAGCTGTTTCATGATGATGACTCGGACC 90
Db 524 GACAGCTCAT-TCATTAATGAGACTCGGACC 551

RESULT 7
US-10-723-860-6888
Sequence 6888, Application US/10723860
Publication No. US20040253606A1

GENERAL INFORMATION:

APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
PRIOR FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6888
LENGTH: 1894
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (650) .. (669)
OTHER INFORMATION: n is a, c, g, or t
US-10-723-860-6888

Query Match 71.3%; Score 64.2; DB 18; Length 1894;
Best Local Similarity 89.9%; Pred. No. 7.6e-15;
Matches 80; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 2 GCTGCATCTTTTCTATGCTCTCCCTGCGCTGATGGAGATACAGACGAAACG 61
DB 435 GCTGCATCTTTTCTATGCTCTCCCTGCTGATGGAGATACAGACGAAACG 494

QY 62 GACAGCTCGTTCATGATGCACTCGGACC 90
DB 495 GACAGCTCAT-TCATATGACTCGGACC 522

RESULT 8
US-10-198-846-11013
; Sequence 11013, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Liilie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinhann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11013
; LENGTH: 2061
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 2, 3, 1831, 1832, 1833, 1834, 1835, 1836, 1837, 1838,
; LOCATION: 1839, 1840, 1841, 1842, 1843, 1844, 1845, 1846, 1847, 1848,
; LOCATION: 1849, 1850, 1851, 1852, 1853, 1854, 1855, 1856, 1860, 2009,
; LOCATION: 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057,
; LOCATION: 2058, 2059, 2060, 2061
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-11013

Query Match 71.3%; Score 64.2; DB 14; Length 2061;
Best Local Similarity 89.9%; Pred. No. 7.8e-15;
Matches 80; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 2 GCTGCATCTTTTCTATGCTCTCCCTGCGCTGATGGAGATACAGACGAAACG 61
DB 427 GCTGCATCTTTTCTATGCTCTCCCTGCTGATGGAGATACAGACGAAACG 486

QY 62 GACAGCTCGTTCATGATGCACTCGGACC 90
DB 487 GACAGCTCAT-TCATATGACTCGGACC 514

RESULT 9
US-10-723-860-2812
; Sequence 2812, Application US/10723860
; Publication No. US20040233606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &

; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NFUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2812
; LENGTH: 1872
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2812

Query Match 69.6%; Score 62.6; DB 18; Length 1872;
Best Local Similarity 88.8%; Pred. No. 3.3e-14;
Matches 79; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 2 GCTGCATCTTTTCTATGCTCTCCCTGCGCTGATGGAGATACAGACGAAACG 61
DB 435 GCTGCATCTTTTCTATGCTCTCCCTGCTGATGGAGATACAGACGAAACG 494

QY 62 GACAGCTCGTTCATGATGCACTCGGACC 90
DB 495 GACAGCTCAT-TCATATGACTCGGACC 522

RESULT 10
US-09-918-995-15342
; Sequence 15342, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15342
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(465)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-15342

Query Match 34.4%; Score 31; DB 10; Length 465;
Best Local Similarity 59.1%; Pred. No. 0.077;
Matches 52; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 2 GCTGCATCTTTTCTATGCTCTCCCTGCGCTGATGGAGATACAGACGAAACG 61
DB 123 GTTTCATGTTCTTGTGACATTCCTCCCTGAGATCAGGTGAGGGTCCAGACACTGACCA 182

QY 62 GACAGCTCGTTCATGATGCACTCGGACC 89
DB 183 GACAGCTTGACAGCTGCTCAAGACGGTC 210

RESULT 11
US-10-425-115-44104
; Sequence 44104, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

```
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5322)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 44104
LENGTH: 449
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_140229C.1
US-10-425-115-44104

Query Match      31.3%; Score 28.2; DB 18; Length 449;
Best Local Similarity 73.5%; Pred. No. 0.98;
Matches 36; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 9 CTTTCTATGCTCTCCCTGCGGCGGCTGATGGAGATACAGACGCA 57
DB 131 CTGTTCTATGCTCTGCGCTGACGCTGACAGAGCGGAGTCTCTCA 179

RESULT 12
US-10-282-122A-42325
Sequence 42325, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Olsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/266,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 42325
LENGTH: 1362
TYPE: DNA
ORGANISM: Yersinia pestis
US-10-282-122A-42325
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Query Match      30.9%; Score 27.8; DB 17; Length 1362;
Best Local Similarity 58.8%; Pred. No. 1.9;
Matches 47; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 11 TTTTCTATGCTCTCCCTGCGGCGGCTGATGGAGATACAGACGCAAGCAGCTCG 70
DB 883 TTGGGTATGGCGGATGCTCTGCTGCTGATTAAGATATCGAAGCAAGTTCACCTGCG 942

QY 71 TMTCATGATGCACTGGACC 90
DB 943 CAAGCGAGAAACTGGCAAC 962

RESULT 13
US-10-322-281-131/c
Sequence 131, Application US/10322281
Publication No. US20040126762A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 52945200100
CURRENT APPLICATION NUMBER: US/10/322,281
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 131
LENGTH: 247461
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(247461)
OTHER INFORMATION: n = A,T,C or G
US-10-322-281-131

Query Match      30.4%; Score 27.4; DB 18; Length 247461;
Best Local Similarity 59.0%; Pred. No. 11;
Matches 46; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 7 ATCTTTCTATGCTCTCCCTGCTGCGGCTGATGGAGATACAGACGCAAGCAG 66
DB 25022 ATCTTACTCTTGCCCTTCTATTGGGTCTACATATGACCTTGCCCTGAGAGCAG 24963

QY 67 CTCGTTTCATGATGACT 84
DB 24962 CCCCATATGAGAGCCACT 24945

RESULT 14
US-09-294-093B-3147
Sequence 3147, Application US/09294093B
Patent No. US20010051335A1
GENERAL INFORMATION:
APPLICANT: Laligudi, Raghunath, V.
APPLICANT: Ito, Laura, Y.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
FILE REFERENCE: PL-0009 US
CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: April 21, 1998
NUMBER OF SEQ ID NOS: 6207
SOFTWARE: PERL Program
SEQ ID NO 3147
LENGTH: 294
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID NO. US20010051335A1 700347266H1
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NAME/KEY: unsure
LOCATION: 44
OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-3147

Query Match 30.0%; Score 27; DB 9; Length 294;
Best Local Similarity 57.1%; Pred. No. 2.6;
Matches 48; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 5 GCATCTTTTCTATGCTCTCCCTGCTGCGCTGATGGAGATACAGACAGCAAAACGAC 64
DB 66 GTATCCTCTTCAAGCTGTGGAGCTGGAGCAGAGAAAGGAGCTATCTTCAAGGC 125
QY 65 AGCTCGTTCATGATGACTCGGA 88
DB 126 ACCTTGCTGATGACGAAGGCGTA 149

RESULT 15

US-10-027-632-161738/c
Sequence 161738, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Mang, David G.
TITLE OR INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ. ID NOS: 325720
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 161738
LENGTH: 745
TYPE: DNA
ORGANISM: Human
US-10-027-632-161738

Query Match 30.0%; Score 27; DB 13; Length 745;
Best Local Similarity 70.6%; Pred. No. 3.3;
Matches 36; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 15 CTAGCTCTCCCTGCTGCGCTGATGGAGATACAGACAGCAAAACGAC 65
DB 155 CTAGACTGTCCCATCTGGGGGTGAGGAGATGACTGACAGTCACTCACTCA 105

Search completed: February 9, 2005, 20:39:52
Job time: 178.371 secs

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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 15:18:20 : Search time 91.3483 Seconds
(without alignments)
2686.875 Million cell updates/sec

Title: US-09-301-507-74_COPY_1_150

Perfect score: 150

Sequence: 1 CGCGCATCTTTTCTATGC.....AGCTCACCCCTGTATACAG 150

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents NA:*

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4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78.8	52.5	1878	4	US-09-620-312D-625
2	28.2	18.8	132871	4	US-09-949-016-13863
3	28.2	18.8	161607	4	US-09-949-016-12210
4	28	18.7	449	4	US-09-621-976-14464
5	27.4	18.3	20975	4	US-09-949-016-15927
6	27.2	18.1	15379	4	US-09-949-016-14191
7	27.2	18.1	19152	4	US-09-949-016-12110
8	27.2	18.1	19153	4	US-09-949-016-15795
9	27.2	18.1	20634	4	US-09-949-016-16627
10	27.2	18.1	4403765	3	US-09-103-840A-2
11	27.2	18.1	4411528	3	US-09-103-840A-1
12	27	18.0	630	4	US-09-854-133-453
13	26.8	17.9	601	4	US-09-949-016-188924
14	26.8	17.9	1362	4	US-09-489-039A-4463
15	26.8	17.9	1362	4	US-09-711-164-178
16	26.8	17.9	1386	4	US-09-489-039A-4437
17	26.8	17.9	1560	4	US-09-489-039A-4420
18	26.8	17.9	27579	4	US-09-949-016-13465
19	26.8	17.9	55328	4	US-09-949-016-12747
20	26.8	17.9	55330	4	US-09-949-016-17146
21	26.8	17.9	76563	4	US-09-949-016-17099
22	26.8	17.9	78269	4	US-09-949-016-12497
23	26.8	17.9	82494	4	US-09-949-016-16937
24	26.8	17.9	4403765	3	US-09-103-840A-2
25	26.8	17.9	4411529	3	US-09-103-840A-1
26	26.6	17.7	601	4	US-09-949-016-50118
27	26.4	17.6	601	4	US-09-949-016-19254

C	28	26.4	17.6	601	4	US-09-949-016-19255	Sequence 19255, A
C	29	26.4	17.6	601	4	US-09-949-016-19256	Sequence 19256, A
C	30	26.4	17.6	601	4	US-09-949-016-131489	Sequence 131489, A
C	31	26.4	17.6	601	4	US-09-949-016-131490	Sequence 131490, A
C	32	26.4	17.6	601	4	US-09-949-016-131491	Sequence 131491, A
C	33	26.4	17.6	1329	1	US-08-278-630A-8	Sequence 8, Appli
C	34	26.4	17.6	9069	4	US-09-949-016-15856	Sequence 15856, A
C	35	26.4	17.6	124700	4	US-09-949-016-11817	Sequence 11817, A
C	36	26.4	17.6	124701	4	US-09-949-016-15439	Sequence 15439, A
C	37	26.2	17.5	450	4	US-09-513-999C-239	Sequence 239, App
C	38	26.2	17.5	1717	4	US-09-949-016-3350	Sequence 3350, App
C	39	26.2	17.5	1952	1	US-08-333-358-1	Sequence 1, Appli
C	40	26.2	17.5	1952	1	US-08-463-694-1	Sequence 1, Appli
C	41	26.2	17.5	1952	1	US-08-698-501-1	Sequence 1, Appli
C	42	26.2	17.5	105733	4	US-09-949-016-13080	Sequence 13080, A
C	43	26.2	17.5	132438	4	US-09-949-016-14349	Sequence 14349, A
C	44	26.2	17.5	132438	4	US-09-949-016-14350	Sequence 14350, A
C	45	26.2	17.5	133719	4	US-09-949-016-15092	Sequence 15092, A

ALIGNMENTS

RESULT 1
US-09-620-312D-625

Sequence 625, Application US/09620312D

Patent No. 6569662

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Asundi, Vinod

APPLICANT: Zhang, Jie

APPLICANT: Ren, Feiyun

APPLICANT: Chen, Rui-hong

APPLICANT: Zhao, Qing A.

APPLICANT: Wehrman, Tom

APPLICANT: Xue, Aidong J.

APPLICANT: Yang, Yonghong

APPLICANT: Wang, Qian-Rui

APPLICANT: Zhou, Ping

APPLICANT: Ma, Yundong

APPLICANT: Wang, Dunrui

APPLICANT: Wang, Zhiwei

APPLICANT: John Tillinghast

APPLICANT: Drmanac, Radoje T.

TITLE OF INVENTION: No. 6569662el Nucleic Acids and

FILE REFERENCE: 784CIP28

CURRENT FILING DATE: 2000-07-19

PRIOR FILING DATE: 2000-07-19

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: 09/488,725

PRIOR FILING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 1105

SOFTWARE: pt_Fl_genes Version 1.0

SEQ ID NO 625

LENGTH: 1878

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (945) .. (1229)

US-09-620-312D-625

Query Match

Best Local Similarity 87.8%; Pred. No. 8.8e-20;

Matches 108; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

2 GCTGCATCTTTTCTATGCTCTCCCTGCGCTGATGGAGATACAGACAGCAACG 61
464 GCTGCATCTTTTCTATGCTCTCCCTGCTGATGGAGATACAGACAGCAACG 523

Qy 62 GACAGCTCGTNTCATGATGACCTCTGCGNCTGATGAGGACCACTATGTTG 121
Db 524 GACAGCTCAT-TCATATGATGACCTGCGACG-CTGCATGAGGACCACTATGTTG 581
Qy 122 NAT 124
Db 582 ATT 584

RESULT 2
US-09-949-016-13863
; Sequence 13863, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13863
; LENGTH: 132871
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(132871)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13863

Query Match 18.8%; Score 28.2; DB 4; Length 132871;
Best Local Similarity 56.0%; Pred. No. 21;
Matches 51; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 13 TTCATGCTCTCCCTGCTGGCGCTGATGAGGATACAGACGAAACGACGCTGCTN 72
Db 106576 TTGACCTCTCTCTTCTGCTTGTTCAGTCTGATGAGAGACGACGATGACCTTTAAT 106635
Qy 73 TCATGATGACTCGACCTCTGCGNCTGCA 103
Db 106636 TCATGTTAGTATGGAAGTACTGGGACTGTA 106666

RESULT 3
US-09-949-016-12210
; Sequence 12210, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12210
; LENGTH: 161607
; TYPE: DNA

; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(161607)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12210

Query Match 18.8%; Score 28.2; DB 4; Length 161607;
Best Local Similarity 56.0%; Pred. No. 23;
Matches 51; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 13 TTCATGCTCTCCCTGCTGGCGCTGATGAGGATACAGACGAAACGACGCTGCTN 72
Db 106576 TTGACCTCTCTCTTCTGCTTGTTCAGTCTGATGAGAGACGACGATGACCTTTAAT 106635
Qy 73 TCATGATGACTCGACCTCTGCGNCTGCA 103
Db 106636 TCATGTTAGTATGGAAGTACTGGGACTGTA 106666

RESULT 4
US-09-621-976-14464
; Sequence 14464, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 14464
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-14464

Query Match 18.7%; Score 28; DB 4; Length 449;
Best Local Similarity 62.3%; Pred. No. 1.5;
Matches 43; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 23 TCCCTGCTGGCGCTGATGAGGATACAGACGAAACGACGCTGNTCATGATGCA 82
Db 243 TCCCTGCTGATGAGTGAAGGGGTCCAGACGCTGACGACGCTTGACAGCTGTCA 302
Qy 83 CTCGACCC 91
Db 303 GACGCTCAC 311

RESULT 5
US-09-949-016-15927/c
; Sequence 15927, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15927

LENGTH: 20975
TYPE: DNA
ORGANISM: Human
US-09-949-016-15927

Query Match
Best Local Similarity 58.2%; Pred. No. 17;
Matches 46; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 26 CTGTGGCGCTGATGGAGATACAGACGAAACGACGCTGCTGATGATGACCTC 85
DB 15721 CAGCTGGCTTATGGGATACAGAGGCCCCCAGGTCAAGCCCTGCCATGAGATC 15662
QY 86 GGACCTCTGCGCTGCTGCT 104
DB 15661 TCCCTCTCCATGATCGCT 15643

RESULT 6
US-09-949-016-14191
Sequence 14191, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14191
LENGTH: 15379
TYPE: DNA
ORGANISM: Human
US-09-949-016-14191

Query Match
Best Local Similarity 54.1%; Pred. No. 18;
Matches 53; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 3 CTGATCTTTTCTATGCTCTCCCTGCGCTGATGGAGATACAGACGAAACGG 62
DB 3888 CTGATCTTTTCTATGCTCTCCCTGCGCTGATGGAGATACAGACGAAACCT 3947
QY 63 ACAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 100
DB 3948 ATGTTGAGAAATAGTAGCTTAGAGACAGTGGATT 3985

RESULT 7
US-09-949-016-12110/c
Sequence 12110, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12110
LENGTH: 19152
TYPE: DNA
ORGANISM: Human
US-09-949-016-12110

Query Match
Best Local Similarity 51.8%; Pred. No. 20;
Matches 59; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 2 GGTGATCTTTTCTATGCTCTCCCTGCGCTGATGGAGATACAGACGAAACG 61
DB 4804 GCGGGGCTTCTGGGGGCGCGGCTGCTCCGCTCTGTTAGGGGAGGTAGGAGTGG 4745
QY 62 GACAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 115
DB 4744 GCGAGCGATCCCAAGTCTCGGGGCGCGGCGGCGGCTCCTCAGGCGCGCT 4691

RESULT 8
US-09-949-016-15795/c
Sequence 15795, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15795
LENGTH: 19153
TYPE: DNA
ORGANISM: Human
US-09-949-016-15795

Query Match
Best Local Similarity 51.8%; Pred. No. 20;
Matches 59; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 2 GGTGATCTTTTCTATGCTCTCCCTGCGCTGATGGAGATACAGACGAAACG 61
DB 4804 GCGGGGCTTCTGGGGGCGCGGCTGCTCCGCTCTGTTAGGGGAGGTAGGAGTGG 4745
QY 62 GACAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 115
DB 4744 GCGAGCGATCCCAAGTCTCGGGGCGCGGCGGCGGCTCCTCAGGCGCGCT 4691

RESULT 9
US-09-949-016-16627
Sequence 16627, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768

RESULT 11
 US-09-103-840A-1/c
 ; Sequence 1, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

```

RESULT 13
US-09-949-016-188924
; Sequence 188924, Application US/09949016
; Patent NO 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

```

;; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: CLO01307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 188924
;; LENGTH: 601
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-188924

Query Match 17.9%; Score 26.8; DB 4; Length 601;
Best Local Similarity 55.7%; Pred. No. 5.2;
Matches 49; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 27 TGCTGGCGCTGATGAGATACAGACAGCAAAACGACGCTCGTTCATGATGACTCG 86
DB 192 TGCTGCCCTTGGGGGACATGAGCGCACCAAGACCCCTCGCGCTCATCCACCAAGG 251

QY 87 GACCTCTCGCCTGATGAGACAC 114
DB 252 AACCCAAAGCGCCCTCTCCGCGAGAAC 279

RESULT 14

US-09-489-039A-4463/C
;; Sequence 4463, Application US/09489039A
;; Patent No. 6610836
;; GENERAL INFORMATION:
;; APPLICANT: Gary Breton et. al
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;; FILE REFERENCE: 2709.2004001
;; CURRENT APPLICATION NUMBER: US/09/489,039A
;; CURRENT FILING DATE: 2000-01-27
;; PRIOR APPLICATION NUMBER: US 60/117,747
;; PRIOR FILING DATE: 1999-01-29
;; NUMBER OF SEQ ID NOS: 14342
;; SEQ ID NO 4463
;; LENGTH: 684
;; TYPE: DNA
;; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-4463

Query Match 17.9%; Score 26.8; DB 4; Length 684;
Best Local Similarity 68.5%; Pred. No. 5.5;
Matches 37; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 17 ATGCTCTCCCTGCTGGCGCTGATGAGATACAGACAGCAAAACGACGCTCG 70
DB 473 ATGGCGACGTGCTGCTGCTGATTGAAGATATCGAGAGCAAGTTGACCGCGCG 420

RESULT 15

US-09-711-164-178
;; Sequence 178, Application US/09711164
;; Patent No. 6589738
;; GENERAL INFORMATION:
;; APPLICANT: Forsyth, R. Allyn
;; APPLICANT: Ohlsen, Kari
;; APPLICANT: Zykand, Judith
;; TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THEREOF
;; FILE REFERENCE: ELITRA.008A
;; CURRENT APPLICATION NUMBER: US/09/711,164
;; CURRENT FILING DATE: 2000-11-09
;; PRIOR APPLICATION NUMBER: US 60/164415

;; PRIOR FILING DATE: 1999-11-9
;; NUMBER OF SEQ ID NOS: 469
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 178
;; LENGTH: 1362
;; TYPE: DNA
;; ORGANISM: Escherichia coli
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1)...(1362)
US-09-711-164-178

Query Match 17.9%; Score 26.8; DB 4; Length 1362;
Best Local Similarity 68.5%; Pred. No. 7.7;
Matches 37; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 17 ATGCTCTCCCTGCTGGCGCTGATGAGATACAGACAGCAAAACGACGCTCG 70
DB 889 ATGGCGACGTACTGTGCTGCTGATGAGATATCGAAGCAAAAGTTGACCGCGCG 942

Search completed: February 9, 2005, 18:15:35
Job time : 99.3483 secs

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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 17:59:05 ; Search time 295.618 Seconds
(without alignments)
2920.530 Million cell updates/sec

Title: US-09-301-507-74_COPY_1_150
Perfect score: 150
Sequence: 1 CGCGCATCTTTTCTATGC.....AGCTCACCCCTGTATACAG 150

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 433806 seqs, 2877871033 residues

Total number of hits satisfying chosen parameters: 8627612

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

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5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09C_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
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22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	146	97.3	336	US-10-355-716-74	Sequence 74, App1
2	86.8	57.9	252	US-10-355-716-76	Sequence 76, App1
3	79.8	53.2	412	US-10-198-846-1775	Sequence 1775, Ap
4	78.8	52.5	455	US-10-198-846-8657	Sequence 8657, Ap
5	78.8	52.5	1878	US-10-037-720-625	Sequence 625, App
6	78.8	52.5	1878	US-10-117-722-625	Sequence 625, App
7	78.8	52.5	2061	US-10-198-846-11013	Sequence 11013, A
8	78	52.0	1894	US-10-723-860-6888	Sequence 6888, Ap
9	77.2	51.5	1872	US-10-723-860-2812	Sequence 2812, Ap
10	32.4	21.6	1334	US-10-437-963-83624	Sequence 83624, A
11	31.4	20.9	465	US-09-918-995-15342	Sequence 15342, A

C 12	31.2	20.8	260	18	US-10-425-115-31593	Sequence 31593, A
13	29.8	19.9	614	18	US-10-767-701-23603	Sequence 23603, A
14	29.8	19.9	1820	18	US-10-676-2488-1	Sequence 1, App1
15	29.4	19.6	758	17	US-10-425-114-9467	Sequence 9467, App
16	29.4	19.6	946	17	US-10-374-780A-1592	Sequence 1592, Ap
17	29.4	19.6	946	17	US-10-412-6998-1638	Sequence 1638, Ap
18	29.4	19.6	1419	17	US-10-424-599-17436	Sequence 17436, A
19	29	19.3	245	19	US-10-480-587-23	Sequence 23, App1
20	28.6	19.1	793	13	US-10-027-632-16464	Sequence 16464, A
C 21	28.6	19.1	793	17	US-10-027-632-16464	Sequence 16464, A
22	28.4	18.9	219	18	US-10-437-963-7315	Sequence 7315, Ap
23	28.2	18.8	285	18	US-10-425-115-20005	Sequence 20005, A
24	28.2	18.8	449	18	US-10-425-115-44104	Sequence 44104, A
25	28	18.7	294	9	US-09-294-003B-3147	Sequence 3147, Ap
C 26	28	18.7	631	13	US-10-027-632-307934	Sequence 307934, A
C 27	28	18.7	631	13	US-10-027-632-307935	Sequence 307935, A
C 28	28	18.7	631	13	US-10-027-632-307936	Sequence 307936, A
C 29	28	18.7	631	17	US-10-027-632-307934	Sequence 307934, A
C 30	28	18.7	631	17	US-10-027-632-307935	Sequence 307935, A
C 31	28	18.7	631	17	US-10-027-632-307936	Sequence 307936, A
32	28	18.7	1386	17	US-10-425-114-2994	Sequence 2994, Ap
33	28	18.7	1602	18	US-10-739-930-1655	Sequence 1655, Ap
34	28	18.7	1904	17	US-10-388-934-237	Sequence 237, App
35	28	18.7	1983	18	US-10-425-115-184377	Sequence 184377, A
36	28	18.7	3936	18	US-10-437-963-22944	Sequence 22944, A
C 37	27.8	18.5	220	16	US-10-029-386-18087	Sequence 18087, A
C 38	27.8	18.5	557	16	US-10-029-386-4387	Sequence 4387, Ap
C 39	27.8	18.5	1362	17	US-10-282-122A-42325	Sequence 42325, A
C 40	27.8	18.5	822900	17	US-10-292-798-1393	Sequence 1393, Ap
41	27.6	18.4	264	18	US-10-425-115-132450	Sequence 132450, A
C 42	27.6	18.4	1964	17	US-10-425-114-25149	Sequence 25149, A
C 43	27.6	18.4	2647	18	US-10-425-115-120423	Sequence 120423, A
44	27.6	18.4	56258	13	US-10-087-192-913	Sequence 913, App
C 45	27.4	18.3	247461	18	US-10-322-281-131	Sequence 131, App

ALIGNMENTS

RESULT 1
US-10-355-716-74
Sequence 74, Application US/10355716
Publication No. US20030216339A1
GENERAL INFORMATION:
APPLICANT: Cynader, Max
Prasad, Shiy
TITLE OF INVENTION: GENE SEQUENCES ASSOCIATED WITH NEURAL PLASTICITY AND METHODS RELATED THERETO
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/355,716
FILING DATE: 31-Jan-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/301,507
FILING DATE: 28-Apr-1999
ATTORNEY/AGENT INFORMATION:
NAME: Potler, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 230018.401C1
TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-10-355-716-74

Query Match 97.3%; Score 146; DB 17; Length 336;
Best Local Similarity 100.0%; Pred. No. 3.1e-46;
Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCTGATCTTTTCTATGCTCTCCCTGCGCTGATGGAGATACAGACGAAAC 60
DB 1 CGCTGATCTTTTCTATGCTCTCCCTGCGCTGATGGAGATACAGACGAAAC 60
QY 61 GGACAGCTCGTTCATGATGACTGCGACCTCTGCGCTGATGAGGACCACTATGTT 120
DB 61 GGACAGCTCGTTCATGATGACTGCGACCTCTGCGCTGATGAGGACCACTATGTT 120
QY 121 GNATTCTATGACCTGACCCGTTGTAAG 150
DB 121 GNATTCTATGACCTGACCCGTTGTAAG 150

RESULT 2

US-10-355-716-76
Sequence 76, Application US/10355716
Publication No. US20030216339A1

GENERAL INFORMATION:

APPLICANT: Cynader, Max
Praad, Shiv
TITLE OF INVENTION: GENE SEQUENCES ASSOCIATED WITH NEURAL
PLASTICITY AND METHODS RELATED THERETO
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESS: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/355,716
FILING DATE: 31-Jan-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/301,507
FILING DATE: 28-Apr-1999
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 230018.401C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 76:

SEQUENCE CHARACTERISTICS:

LENGTH: 252 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 76:

US-10-355-716-76

Query Match 57.9%; Score 86.8; DB 17; Length 252;
Best Local Similarity 96.7%; Pred. No. 3.2e-23;
Matches 88; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGCTGATCTTTTCTATGCTCTCCCTGCGCTGATGGAGATACAGACGAAAC 60
DB 1 CGCTGATCTTTTCTATGCTCTCCCTGCGCTGATGGAGATACAGACGAAAC 60
QY 61 GGACAGCTCGTTCATGATGACTGCGACCTCTGCGCTGATGAGGACCACTATGTT 120
DB 61 GGACAGCTCGTTCATGATGACTGCGACCTCTGCGCTGATGAGGACCACTATGTT 120

RESULT 3

US-10-198-846-1775
Sequence 1775, Application US/10198846
Publication No. US20030099974A1

GENERAL INFORMATION:

APPLICANT: Li, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Steimann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1775
LENGTH: 412
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 3, 203, 293, 343, 398
OTHER INFORMATION: n = A,T,C or G
US-10-198-846-1775

Query Match 53.2%; Score 79.8; DB 14; Length 412;
Best Local Similarity 87.9%; Pred. No. 2e-20;
Matches 109; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

QY 1 CGCTGATCTTTTCTATGCTCTCCCTGCGCTGATGGAGATACAGACGAAAC 60
DB 49 CGCTGATCTTTTCTATGCTCTCCCTGCGCTGATGGAGATACAGACGAAAC 108
QY 61 GGACAGCTCGTTCATGATGACTGCGACCTCTGCGCTGATGAGGACCACTATGTT 120
DB 109 GGACAGCTCAT-TCATATGACTGCGACCTCTGAGC-CTGATGAGGACCACTATGTT 166
QY 121 GNAT 124
DB 167 GATT 170

RESULT 4

US-10-198-846-8657
Sequence 8657, Application US/10198846
Publication No. US20030099974A1

GENERAL INFORMATION:

APPLICANT: Li, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Steimann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846

CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8657
LENGTH: 455
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2, 7, 404, 454
OTHER INFORMATION: n = A,T,C or G
US-10-198-846-8657

Query Match 52.5%; Score 78.8; DB 14; Length 455;
Best Local Similarity 87.8%; Pred. No. 5.1e-20;
Matches 108; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

QY 2 GCTGATCTTTTCTATGCTCTCCCTGCTGGCGCTGATGAGATACAGACGAAACG 61
DB 60 GCTGATCTTTTCTATGCTCTCCCTGCTGGCGATGAGATACAGACGTAACG 119
QY 62 GACAGCTGNTCATGATGACTCGGACCCCTCTGCGNCTGATGAGGACCACTATGTTG 121
DB 120 GACAGCTCAT-TCATATGAGACTCGGACCCCTGAGC-CTGCATGAGGACCACTATGTGG 177
QY 122 NAT 124
DB 178 ATT 180

RESULT 5

US-10-037-270-625
Sequence 625, Application US/10037270
Publication No. US20030104529A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Weinman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunding
APPLICANT: Wang, Duntui
APPLICANT: Wang, Zhiwei
APPLICANT: Tillinghast, John
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/10/037,270
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: pc_FL_genes Version 1.0
SEQ ID NO 625
LENGTH: 1878
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (945) .. (1229)
US-10-037-270-625

Query Match 52.5%; Score 78.8; DB 15; Length 1878;
Best Local Similarity 87.8%; Pred. No. 8.2e-20;
Matches 108; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

QY 2 GCTGATCTTTTCTATGCTCTCCCTGCTGGCGCTGATGAGATACAGACGAAACG 61
DB 464 GCTGATCTTTTCTATGCTCTCCCTGCTGGCGATGAGATACAGACGTAACG 523
QY 62 GACAGCTGNTCATGATGACTCGGACCCCTCTGCGNCTGATGAGGACCACTATGTTG 121
DB 524 GACAGCTCAT-TCATATGAGACTCGGACCCCTGAGC-CTGCATGAGGACCACTATGTGG 581
QY 122 NAT 124
DB 582 ATT 584

RESULT 6

US-10-117-722-625
Sequence 625, Application US/10117722
Publication No. US20030219744A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030219744A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2BCTP
CURRENT APPLICATION NUMBER: US/10/117,722
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: pc_FL_genes Version 1.0
SEQ ID NO 625
LENGTH: 1878
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (945) .. (1229)
US-10-117-722-625

Query Match 52.5%; Score 78.8; DB 17; Length 1878;
Best Local Similarity 87.8%; Pred. No. 8.2e-20;
Matches 108; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

QY 2 GCTGATCTTTTCTATGCTCTCCCTGCTGGCGCTGATGAGGAGATACAGACGAAACG 61
DB 464 GCTGATCTTTTCTATGCTCTCCCTGCTGGCGATGAGGAGATACAGACGTAACG 523
QY 62 GACAGCTGNTCATGATGACTCGGACCCCTCTGCGNCTGATGAGGACCACTATGTTG 121
DB 524 GACAGCTCAT-TCATATGAGACTCGGACCCCTGAGC-CTGCATGAGGACCACTATGTGG 581
QY 122 NAT 124
DB 582 ATT 584

RESULT 7

US-10-198-846-11013
Sequence 11013, Application US/10198846
Publication No. US2003009974A1
GENERAL INFORMATION:
APPLICANT: Lillie, James

APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11013
LENGTH: 2061
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 1, 2, 3, 1831, 1832, 1833, 1834, 1835, 1836, 1837, 1838,
LOCATION: 1839, 1840, 1841, 1842, 1843, 1844, 1845, 1846, 1847, 1848,
LOCATION: 1849, 1850, 1851, 1852, 1853, 1854, 1855, 1856, 1860, 2009,
LOCATION: 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047
OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc feature
LOCATION: 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057,
LOCATION: 2058, 2059, 2060, 2061
OTHER INFORMATION: n = A,T,C or G
US-10-198-846-11013

Query Match 52.5%; Score 78.8; DB 14; Length 2061;
Best Local Similarity 87.8%; Pred. No. 8.5e-20;
Matches 108; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

QY 2 GGTGATCTTTTCTATGCTCTCCCTGCTGCGCTGATGGAGATACAGACAGAAAACG 61
DB 427 GCTGCATCTTTTCTATGCTCTCCCTGCTGCGCTGATGGAGATACAGAGTAAACG 486
QY 62 GACAGCTGTTTCATGATGATGACCTGCGACCTCTGCGTGCATGAGGACCACTATGTTG 121
DB 487 GACAGCTCAT-TCATATGAGACTCGGACCTCGACG-CTGCATGAGGACCACTATGTTG 544
QY 122 NAT 124
DB 545 ATT 547

RESULT 8
US-10-723-860-6888
Sequence 6888, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6888
LENGTH: 1894
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (650)..(669)
OTHER INFORMATION: n is a, c, g, or t

US-10-723-860-6888

Query Match 52.0%; Score 78; DB 18; Length 1894;
Best Local Similarity 89.8%; Pred. No. 1.7e-19;
Matches 106; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

QY 2 GGTGATCTTTTCTATGCTCTCCCTGCTGCGCTGATGGAGATACAGACAGAAAACG 61
DB 435 GCTGCATCTTTTCTATGCTCTCCCTGCTGCGCTGATGGAGATACAGAGTAAACG 494
QY 62 GACAGCTGTTTCATGATGATGACCTGCGACCTCTGCGTGCATGAGGACCACTATGTTG 119
DB 495 GACAGCTCAT-TCATATGAGACTCGGACCTCGACG-CTGCATGAGGACCACTATGTTG 550

RESULT 9
US-10-723-860-2812
Sequence 2812, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2812
LENGTH: 1872
TYPE: DNA
ORGANISM: Homo sapiens
US-10-723-860-2812

Query Match 51.5%; Score 77.2; DB 18; Length 1872;
Best Local Similarity 87.0%; Pred. No. 3.4e-19;
Matches 107; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

QY 2 GGTGATCTTTTCTATGCTCTCCCTGCTGCGCTGATGGAGATACAGACAGAAAACG 61
DB 435 GCTGCATCTTTTCTATGCTCTCCCTGCTGCGCTGATGGAGATACAGAGTAAACG 494
QY 62 GACAGCTGTTTCATGATGATGACCTGCGACCTCTGCGTGCATGAGGACCACTATGTTG 121
DB 495 GACAGCTCAT-TCATATGAGACTCGGACCTCGACG-CTGCATGAGGACCACTATGTTG 552
QY 122 NAT 124
DB 553 ATT 555

RESULT 10
US-10-437-963-83624/C
Sequence 83624, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14

```
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 83624
/ LENGTH: 1334
/ TYPE: DNA
/ ORGANISM: Oryza sativa
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_82938C.1
US-10-437-963-83624
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Query Match
Best Local Similarity 21.6%; Score 32.4; DB 18; Length 1334;
Best Local Similarity 58.1%; Pred. No. 0.086;
Matches 54; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
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```
QY 36 TCATGGAGATACAGACAGCAAAACGACGCTGTCATGATGACGCGACCTCTG 95
DB 511 TGAAGGCTGTTTCAGAGCAAAATCCCACTTCCTACTGACTCAATCTCAGCTCCG 452
QY 96 CGNCTGATGAGGACCACTATGTTGATTTA 128
DB 451 CGGGGCGATGAAGCAATGTGTGATCCCA 419
```

RESULT 11

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US-09-918-995-15342
/ Sequence 15342, Application US/09918995
/ Publication No. US20030073623A1
```

```
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Hyseq, Inc.
```

```
/ TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
```

```
/ FILE REFERENCE: 20411-756
```

```
/ CURRENT APPLICATION NUMBER: US/09/918,995
```

```
/ PRIOR FILING DATE: 2001-07-30
```

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/ PRIOR APPLICATION NUMBER: US/09/235,076
```

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/ NUMBER OF SEQ ID NOS: 38054
```

```
/ SOFTWARE: FastSeq for Windows Version 3.0
```

```
/ SEQ ID NO 15342
```

```
/ LENGTH: 465
```

```
/ TYPE: DNA
```

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/ ORGANISM: Homo sapiens
```

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/ FEATURE:
```

```
/ NAME/KEY: misc.feature
```

```
/ LOCATION: (1)-(465)
```

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/ OTHER INFORMATION: n = A,T,C or G
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```
US-09-918-995-15342
```

```
Query Match
Best Local Similarity 20.9%; Score 31.4; DB 10; Length 465;
Best Local Similarity 58.9%; Pred. No. 0.15;
Matches 53; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
```

```
QY 2 GCTGCATCTTTTCTATGCTCTCCCTGCTGGCGCTGATGGAGATACAGACGAAACG 61
DB 123 GTTATGATGTTCTTGACACTTCCCTCTGGGATCAGGTGAGGGGTCAGACGCTGACA 182
QY 62 GACAGCTGTTTCATGATGATCGACTCGACCC 91
DB 183 GACAGCTTGACAGCTGTGTAAGAGCGTCA 212
```

RESULT 12

```
US-10-425-115-31593/C
```

```
/ Sequence 31593, Application US/10425115
```

```
/ Publication No. US2004021472A1
```

```
/ GENERAL INFORMATION:
```

```
/ APPLICANT: La Rosa, Thomas J.
```

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/ APPLICANT: Kovalic, David K.
```

```
/ APPLICANT: Zhou, Yihua
```

```
/ APPLICANT: Cao, Yongwei
```

```
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
```

```
/ FILE REFERENCE: 38-21(53222)B
```

```
/ CURRENT APPLICATION NUMBER: US/10/425,115
```

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/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 31593
/ LENGTH: 260
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
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/ OTHER INFORMATION: Clone ID: MRT4577_128824C.1
US-10-425-115-31593
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Query Match
Best Local Similarity 20.8%; Score 31.2; DB 18; Length 260;
Best Local Similarity 55.9%; Pred. No. 0.15;
Matches 57; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
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QY 13 TTCTATGCTCTCTCCCTGCTGGCGCTGATGGAGATACAGACGAAACGACGCTG 72
DB 128 TTCTCTCCCTGCTCCAGAGATCTGATGAGAAATCCGACACATCGCGATCACACCTC 69
QY 73 TCATGATGACTCGGACCCCTGCGNCTGCATGAGGACACAC 114
DB 68 AATGATACATCTGTAACTTACCAAGAGATGAGTCAAGCC 27
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RESULT 13

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US-10-767-701-23603
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/ Sequence 23603, Application US/10767701
```

```
/ Publication No. US20040172684A1
```

```
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Kovalic, David K.
```

```
/ APPLICANT: Zhou, Yihua
```

```
/ APPLICANT: Cao, Yongwei
```

```
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
```

```
/ FILE REFERENCE: 38-21(53535)B
```

```
/ CURRENT APPLICATION NUMBER: US/10/767,701
```

```
/ PRIOR FILING DATE: 2004-01-29
```

```
/ NUMBER OF SEQ ID NOS: 63128
```

```
/ SEQ ID NO 23603
```

```
/ LENGTH: 614
```

```
/ TYPE: DNA
```

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/ ORGANISM: Sorghum bicolor
```

```
/ FEATURE:
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/ OTHER INFORMATION: Clone ID: 18063385
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US-10-767-701-23603
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Query Match
Best Local Similarity 19.9%; Score 29.8; DB 18; Length 614;
Best Local Similarity 54.2%; Pred. No. 0.68;
Matches 58; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
```

```
QY 2 GCTGCATCTTTTCTATGCTCTCCCTGCTGGCGCTGATGGAGATACAGACGAAACG 61
DB 343 GATGCTTTTCTGACAGATCTCCCTGCTGCTTACTGGAAGATGGAAGCAAAAGC 402
QY 62 GACAGCTGTTTCATGATGATCGAGCTCGACCTCTGAGNCTGATGAG 108
DB 403 TATGCTCTCTGAGAGATCTATGACTGTGATGTTGAGGAG 449
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RESULT 14

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US-10-676-248B-1
```

```
/ Sequence 1, Application US/10676248B
```

```
/ Publication No. US2004016173A1
```

```
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Rogan, Peter
```

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/ APPLICANT: Knoll, Joan
```

```
/ TITLE OF INVENTION: SUBTLEMERIC DNA PROBES AND METHOD OF PRODUCING SAME
```

```
/ FILE REFERENCE: 33026-B
```

```
/ CURRENT APPLICATION NUMBER: US/10/676,248B
```

```
/ PRIOR FILING DATE: 2003-09-30
```

```
/ PRIOR APPLICATION NUMBER: 60/415,345
```

```
/ PRIOR FILING DATE: 2002-09-30
```

```
/ PRIOR APPLICATION NUMBER: 10/676,248
```

```
/ PRIOR FILING DATE: 2003-09-30
```

; PRIOR APPLICATION NUMBER: 60/494,494
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1820
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-676-248B-1

Query Match 19.9%; Score 29.4; DB 18; Length 1820;
Best Local Similarity 53.7%; Pred. No. 0.98;
Matches 58; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

OY 34 GCTGATGGGAGATACAGACAGCAAAACGACAGCTGTTTCATGATGACTCGACCTC 93
DB 197 GTTAAATGACAGAGTTTAACTCAAGGGGACAGATGATCTCAGACAGAAATGACAGACTG 256
OY 94 TGGCNCCTGACATGAGGACCACTATGTTGATTCATGACTCACCCGT 141
DB 257 AGTACACAGAGAGGACGTACCGTACATTTCTTCACCTTTTCTGT 304

RESULT 15

US-10-425-114-9467
; Sequence 9467, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 9467
; LENGTH: 758
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700848185_FLI
US-10-425-114-9467

Query Match 19.6%; Score 29.4; DB 17; Length 758;
Best Local Similarity 63.6%; Pred. No. 1;
Matches 42; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

OY 80 CGACTCGAGCCTCTGCAGTGCATGAGCAGCAGCACTATGTTGATTCATGACTCACCC 139
DB 317 CGCAGCGTTCCCTCTGACATGCGGAGAGCTGCTGCCACACTACTAGGTCAACCC 376
OY 140 GTTGAT 145
DB 377 CTTGTT 382

Search completed: February 9, 2005, 20:39:54
Job time : 297.618 secs

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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 18:10:40 ; Search time 106 Seconds
(without alignments)
2392.669 Million cell updates/sec

Title: US-09-301-507-74_COPY_1_155
Sequence: 1 CGCGCATCTTTTCTATGC.....ACCCGTTGNTACAAGTGTAG 155

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	22	14.2	1878	4	US-09-620-312D-625
2	20	12.9	1895	3	US-09-326-203A-14
3	20	12.9	1976	3	US-09-165-042-2
4	20	12.9	2803	4	US-09-949-016-2464
5	20	12.9	4237	4	US-09-949-016-649
6	20	12.9	107941	4	US-09-949-016-14206
7	20	12.9	109378	4	US-09-949-016-12391
8	19	12.3	939	4	US-09-489-039A-1843
9	18	11.6	885	4	US-09-902-540-5476
10	18	11.6	29899	4	US-09-902-540-1265
11	17	11.0	601	4	US-09-949-016-168695
12	17	11.0	1512	4	US-09-252-991A-5614
13	17	11.0	2079	4	US-09-252-991A-5584
14	17	11.0	2436	4	US-09-252-991A-5645
15	17	11.0	30635	4	US-09-949-016-16501
16	17	11.0	200663	4	US-09-949-016-12559
17	16	10.3	390	4	US-09-489-039A-887
18	16	10.3	518	4	US-09-621-976-18442
19	16	10.3	651	4	US-09-489-039A-94
20	16	10.3	771	4	US-09-489-039A-4386
21	16	10.3	960	4	US-09-489-039A-4989
22	16	10.3	1023	4	US-09-489-039A-754
23	16	10.3	1149	4	US-09-489-039A-3580
24	16	10.3	1194	4	US-09-489-039A-5491
25	16	10.3	1235	1	US-08-095-726-13
26	16	10.3	1235	1	US-08-095-726-15
27	16	10.3	1235	1	US-08-096-623A-13

28	16	10.3	1235	1	US-08-096-623A-15	Sequence 15, Appl
29	16	10.3	1266	4	US-09-489-039A-812	Sequence 812, App
30	16	10.3	1950	4	US-09-489-039A-4709	Sequence 4709, Ap
31	16	10.3	12655	4	US-09-252-991A-10136	Sequence 10136, A
32	16	10.3	5737	1	US-08-259-264-1	Sequence 1, Appl1
33	16	10.3	8114	3	US-09-453-702B-29	Sequence 29, Appl
34	16	10.3	10095	3	US-08-822-586-45	Sequence 45, Appl
35	16	10.3	14545	4	US-09-949-016-15986	Sequence 15986, A
36	16	10.3	37288	4	US-09-949-016-14593	Sequence 14593, A
37	16	10.3	37288	4	US-09-949-016-14594	Sequence 14594, A
38	16	10.3	67899	4	US-09-949-016-15432	Sequence 15432, A
39	16	10.3	67902	4	US-09-949-016-11870	Sequence 11870, A
40	16	10.3	84558	4	US-09-949-016-15752	Sequence 15752, A
41	16	10.3	94987	4	US-09-949-016-12510	Sequence 12510, A
42	16	10.3	1830121	4	US-09-557-884-1	Sequence 1, Appl1
43	16	10.3	1830121	4	US-09-643-990A-1	Sequence 1, Appl1
44	16	10.3	4403765	3	US-09-103-840A-2	Sequence 2, Appl1
45	16	10.3	4411529	3	US-09-103-840A-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-620-312D-625

Sequence 625, Application US/09620312D
Patent No. 6569662

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Asundi, Vinod

APPLICANT: Zhen, Jie

APPLICANT: Ren, Feiyan

APPLICANT: Chen, Rui-hong

APPLICANT: Zhao, Qing A.

APPLICANT: Wehrman, Tom

APPLICANT: Xue, Aidong J.

APPLICANT: Yang, Yonghong

APPLICANT: Wang, Jiah-Rui

APPLICANT: Zhou, Ping

APPLICANT: Ma, Yungling

APPLICANT: Wang, Duntui

APPLICANT: Wang, Zhilwei

APPLICANT: John Tillinghast

APPLICANT: Drmanac, Radoje T.

TITLE OF INVENTION: No. 6569662el Nucleic Acids and

FILE REFERENCE: 784CIP2B

CURRENT APPLICATION NUMBER: US/09/620,312D

PRIOR FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: 09/488,725

NUMBER OF SEQ ID NOS: 1105

SOFTWARE: PC FL genes Version 1.0

SEQ ID NO 625

LENGTH: 1878

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (945) .. (1229)

US-09-620-312D-625

Query Match

Best local Similarity 100.0%; Pred. No. 0.008;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 473 TTTCTATGCTCTCCCTGCTGG 32

11 TTTCTATGCTCTCCCTGCTGG 32

RESULT 2
US-09-326-203A-14
; Sequence 14, Application US/09326203A
; Patent No. 6444876
; GENERAL INFORMATION:
; APPLICANT: Lashner, Mike
; APPLICANT: Ruzinskiy, Diane
; TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
; TITLE OF INVENTION: Acid Sequences
; FILE REFERENCE: 17045/00/NO
; CURRENT APPLICATION NUMBER: US/09/326,203A
; CURRENT FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 60/088,143
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/108,389
; PRIOR FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1895
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc feature
; LOCATION: (209)
; OTHER INFORMATION: n at position 209 is unknown
US-09-326-203A-14

Query Match 12.9%; Score 20; DB 3; Length 1895;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CTCCTGCTGCGCTGATGG 41
DB 524 CTCCTGCTGCGCTGATGG 543
RESULT 3
US-09-165-042-2
; Sequence 2, Application US/09165042
; Patent No. 6100077
; GENERAL INFORMATION:
; APPLICANT: Sturley, Stephen L.
; APPLICANT: Oelkers, Peter
; TITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL
; TITLE OF INVENTION: ACYLTRANSFERASE
; FILE REFERENCE: 0575/56331
; CURRENT APPLICATION NUMBER: US/09/165,042
; CURRENT FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1976
; TYPE: DNA
; ORGANISM: Yeast
US-09-165-042-2

Query Match 12.9%; Score 20; DB 3; Length 1976;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CTCCTGCTGCGCTGATGG 41
DB 823 CTCCTGCTGCGCTGATGG 842

RESULT 4
US-09-949-016-2464
; Sequence 2464, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2464
; LENGTH: 2803
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2464

Query Match 12.9%; Score 20; DB 4; Length 2803;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 CTCGTGCGCTGATGGAGA 45
DB 1720 CTCGTGCGCTGATGGAGA 1739

RESULT 5
US-09-949-016-649
; Sequence 649, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 649
; LENGTH: 4237
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-649

Query Match 12.9%; Score 20; DB 4; Length 4237;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 CTCGTGCGCTGATGGAGA 45
DB 1725 CTCGTGCGCTGATGGAGA 1744

RESULT 6
US-09-949-016-14206
; Sequence 14206, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 14206
 LENGTH: 107941
 TYPE: DNA
 ORGANISM: Human
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(107941)
 OTHER INFORMATION: n = A,T,C or G
 US-09-949-016-14206

Query Match 12.9%; Score 20; DB 4; Length 107941;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 CTGCTGGCGCTGATGGAGA 45
 Db 74396 CTGCTGGCGCTGATGGAGA 74415

RESULT 7
 US-09-949-016-12391
 Sequence 12391, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 12391
 LENGTH: 109378
 TYPE: DNA
 ORGANISM: Human
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(109378)
 OTHER INFORMATION: n = A,T,C or G
 US-09-949-016-12391

Query Match 12.9%; Score 20; DB 4; Length 109378;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 CTGCTGGCGCTGATGGAGA 45
 Db 74401 CTGCTGGCGCTGATGGAGA 74420

RESULT 8
 US-09-489-039A-1843
 Sequence 1843, Application US/09489039A
 Patent No. 6610836
 GENERAL INFORMATION:
 APPLICANT: Gary Bretton et. al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709,2004001
 CURRENT APPLICATION NUMBER: US/09/489,039A
 CURRENT FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: US 60/117,747
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 14342
 SEQ ID NO 1843
 LENGTH: 939
 TYPE: DNA
 ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-1843

Query Match 12.3%; Score 19; DB 4; Length 939;
 Best Local Similarity 100.0%; Pred. No. 0.43;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TGCTGGCGCTGATGGAGA 45
 Db 377 TGCTGGCGCTGATGGAGA 395

RESULT 9
 US-09-902-540-5476
 Sequence 5476, Application US/09902540
 Patent No. 6833447
 GENERAL INFORMATION:
 APPLICANT: Goldman, Barry S.
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Wiegand, Roger C.
 TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 FILE REFERENCE: 38-10(115849)B
 CURRENT APPLICATION NUMBER: US/09/902,540
 CURRENT FILING DATE: 2001-07-10
 PRIOR APPLICATION NUMBER: 60/217,883
 PRIOR FILING DATE: 2000-07-10
 NUMBER OF SEQ ID NOS: 16825
 SEQ ID NO 5476
 LENGTH: 885
 TYPE: DNA
 ORGANISM: Myxococcus xanthus
 US-09-902-540-5476

Query Match 11.6%; Score 18; DB 4; Length 885;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 CCTGCTGGCGCTGATGGG 42
 Db 525 CCTGCTGGCGCTGATGGG 542

RESULT 10
 US-09-902-540-1265
 Sequence 1265, Application US/09902540
 Patent No. 6833447
 GENERAL INFORMATION:
 APPLICANT: Goldman, Barry S.
 APPLICANT: Hinkle, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Wiegand, Roger C.
 TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 FILE REFERENCE: 38-10(115849)B
 CURRENT APPLICATION NUMBER: US/09/902,540
 CURRENT FILING DATE: 2001-07-10
 PRIOR APPLICATION NUMBER: 60/217,883
 PRIOR FILING DATE: 2000-07-10
 NUMBER OF SEQ ID NOS: 16825
 SEQ ID NO 1265
 LENGTH: 29899
 TYPE: DNA
 ORGANISM: Myxococcus xanthus
 US-09-902-540-1265

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Query Match      11.6%; Score 18; DB 4; Length 29899;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      25 CCTGCTGGCGCTGATGG 42
DB      29492 CCTGCTGGCGCTGATGG 29509

RESULT 11
US-09-949-016-168695
; Sequence 168695, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 168695
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-168695

Query Match      11.0%; Score 17; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      18 TGCTCTCCCTGCTGGCG 34
DB      585 TGCTCTCCCTGCTGGCG 601

RESULT 12
US-09-252-991A-5614
; Sequence 5614, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5614
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5614

Query Match      11.0%; Score 17; DB 4; Length 1512;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      25 CCTGCTGGCGCTGATGG 41
DB      655 CCTGCTGGCGCTGATGG 671

Query Match      11.0%; Score 17; DB 4; Length 2079;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      25 CCTGCTGGCGCTGATGG 41
DB      232 CCTGCTGGCGCTGATGG 216

RESULT 13
US-09-252-991A-5584/c
; Sequence 5584, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5584
; LENGTH: 2079
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5584

Query Match      11.0%; Score 17; DB 4; Length 2436;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      25 CCTGCTGGCGCTGATGG 41
DB      888 CCTGCTGGCGCTGATGG 904

RESULT 14
US-09-252-991A-5645
; Sequence 5645, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5645
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5645

Query Match      11.0%; Score 17; DB 4; Length 2436;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      25 CCTGCTGGCGCTGATGG 41
DB      888 CCTGCTGGCGCTGATGG 904

RESULT 15
US-09-949-016-16501
; Sequence 16501, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
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; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO: 16501
 ; LENGTH: 30635
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-949-016-16501

Query Match 11.0%; Score 17; DB 4; Length 30635;
 Best Local Similarity 100.0%; Pred. No. 8.2;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 TGCTCTCCCTGCTGCG 34
 Db 20557 TGCTCTCCCTGCTGCG 20573

Search completed: February 9, 2005, 23:47:33
 Job time : 110 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2005, 20:25:15 ; Search time 273 Seconds
(without alignments)
3267.912 Million cell updates/sec

Title: US-09-301-507-74_COPY_1_155

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Gapex 60.0, Gapext 60.0

Searched: 4313806 seqs, 287871033 residues

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Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database: Published Applications NA:*

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22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	155	100.0	336	17	US-10-355-716-74
2	71	45.8	252	17	US-10-355-716-76
3	22	14.2	412	14	US-10-198-846-1775
4	22	14.2	455	14	US-10-198-846-8657
5	22	14.2	1872	18	US-10-723-860-2812
6	22	14.2	1878	15	US-10-037-270-625
7	22	14.2	1878	17	US-10-117-722-625
8	22	14.2	1894	18	US-10-723-860-6888
9	22	14.2	2061	14	US-10-198-846-11013
10	20	12.9	371	9	US-09-867-701-5894
11	20	12.9	457	9	US-09-867-701-2415

12	20	12.9	1411	14	US-10-273-438-1	Sequence 1, Appli
13	20	12.9	1411	16	US-10-040-315A-1	Sequence 1, Appli
14	20	12.9	1411	17	US-10-659-800-1	Sequence 1, Appli
15	20	12.9	1467	15	US-10-278-733-2	Sequence 2, Appli
16	20	12.9	1467	15	US-10-278-733-9	Sequence 9, Appli
17	20	12.9	1895	13	US-10-157-855-14	Sequence 14, Appli
18	20	12.9	1976	18	US-10-717-897-47	Sequence 47, Appli
19	20	12.9	1976	18	US-10-394-808-4	Sequence 4, Appli
20	20	12.9	1976	18	US-10-803-482-4	Sequence 4, Appli
21	20	12.9	4237	10	US-09-962-832-117	Sequence 117, App
22	20	12.9	4237	10	US-09-873-367C-319	Sequence 319, App
23	23	12.3	927	17	US-10-282-122A-23461	Sequence 23461, A
24	18	11.6	298	18	US-10-767-701-19315	Sequence 19335, A
25	18	11.6	96597	17	US-10-052-482-103	Sequence 103, App
26	17	11.0	257	9	US-09-864-761-30713	Sequence 30713, A
27	17	11.0	382	9	US-09-864-761-14158	Sequence 14158, A
28	17	11.0	419	9	US-09-864-761-16753	Sequence 16753, A
29	17	11.0	475	9	US-09-864-761-14992	Sequence 14992, A
30	17	11.0	931	17	US-10-424-859-129252	Sequence 129252, A
31	17	11.0	2442	17	US-10-282-122A-15579	Sequence 15579, A
32	17	11.0	119241	18	US-10-684-422-97	Sequence 97, Appli
33	17	11.0	216929	18	US-10-741-601-5727	Sequence 5727, Ap
34	17	11.0	224112	18	US-10-367-094-80	Sequence 80, Appli
35	16	10.3	201	18	US-10-719-893-24114	Sequence 24114, A
36	16	10.3	201	18	US-10-719-893-24525	Sequence 24525, A
37	16	10.3	312	18	US-10-357-930-1847	Sequence 1847, Ap
38	16	10.3	343	17	US-10-242-535A-38655	Sequence 38655, A
39	16	10.3	343	17	US-10-085-783A-38655	Sequence 38655, A
40	16	10.3	395	16	US-09-803-719-1193	Sequence 1193, Ap
41	16	10.3	399	10	US-09-803-719-816	Sequence 816, App
42	16	10.3	403	9	US-09-918-995-5789	Sequence 5789, Ap
43	16	10.3	403	9	US-09-960-352-739	Sequence 739, App
44	16	10.3	410	18	US-10-357-530-11016	Sequence 11016, A
45	16	10.3	412	18	US-10-425-115-59275	Sequence 59275, A

ALIGNMENTS

RESULT 1
US-10-355-716-74
Sequence 74, Application US/10355716
Publication No. US20030215339A1
GENERAL INFORMATION:
APPLICANT: Cynader, Max
TITLE OF INVENTION: GENE SEQUENCES ASSOCIATED WITH NEURAL PLASTICITY AND METHODS RELATED THERETO
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESS: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/355, 716
FILING DATE: 31-Jan-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/301,507
FILING DATE: 28-Apr-1999
ATTORNEY/AGENT INFORMATION:
NAME: Poter, Jane E., R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 230018, 401C1
TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-10-355-716-74

Query Match 100.0%; Score 155; DB 17; Length 336;
Best Local Similarity 100.0%; Pred. No. 5.1e-79;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCTGCACTTTTTCATGCTCTCCCTGCTGGCGCTGATGGAGATACAGACAGCAAAAC 60
DB 1 CGCTGCACTTTTTCATGCTCTCCCTGCTGGCGCTGATGGAGATACAGACAGCAAAAC 60
QY 61 GGACAGCTCGTTCATGATGACCTGGACCCCTGCGCCTGATGAGGATACAGACAGCAAAAC 120
DB 61 GGACAGCTCGTTCATGATGACCTGGACCCCTGCGCCTGATGAGGATACAGACAGCAAAAC 120
QY 121 GNAATTCATGAGCTCACCCGTTGATACAGAGTAG 155
DB 121 GNAATTCATGAGCTCACCCGTTGATACAGAGTAG 155

RESULT 2
US-10-355-716-76
Sequence 76, Application US/10355716
Publication No. US20030216339A1
GENERAL INFORMATION:
APPLICANT: Cynader, Max
Prasad, Shriv

TITLE OF INVENTION: GENE SEQUENCES ASSOCIATED WITH NEURAL
PLASTICITY AND METHODS RELATED THERETO
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group PLLC
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/355, 716
FILING DATE: 31-Jan-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/301,507
FILING DATE: 28-Apr-1999
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 230018,401C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 76:
US-10-355-716-76

Query Match 45.8%; Score 71; DB 17; Length 252;
Best Local Similarity 100.0%; Pred. No. 1.5e-30;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCTGCACTTTTTCATGCTCTCCCTGCTGGCGCTGATGGAGATACAGACAGCAAAAC 60
DB 1 CGCTGCACTTTTTCATGCTCTCCCTGCTGGCGCTGATGGAGATACAGACAGCAAAAC 60
QY 61 GGACAGCTCGT 71
DB 61 GGACAGCTCGT 71

RESULT 3
US-10-198-846-1775
Sequence 1775, Application US/10198846
Publication No. US2003009974A1
GENERAL INFORMATION:
APPLICANT: Liilie, James

APPLICANT: Xu, Yongyao
Wang, Youzhen
APPLICANT: Steinhmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198, 846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306, 220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1775

LENGTH: 412
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 3, 203, 293, 398
OTHER INFORMATION: n = A,T,C or G

US-10-198-846-1775

Query Match 14.2%; Score 22; DB 14; Length 412;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TTTTCTATGCTCTCCCTGCTGG 32
DB 59 TTTTCTATGCTCTCCCTGCTGG 80

RESULT 4
US-10-198-846-8657
Sequence 8657, Application US/10198846
Publication No. US2003009974A1
GENERAL INFORMATION:
APPLICANT: Liilie, James

APPLICANT: Xu, Yongyao
Wang, Youzhen
APPLICANT: Steinhmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198, 846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306, 220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8657

LENGTH: 455
TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2, 7, 404, 454
OTHER INFORMATION: n = A,T,C or G
US-10-198-846-8657

Query Match 14.2% Score 22; DB 14; Length 455;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TTTTCTATGCTCTCCCTGCTGG 32
|||||
Db 69 TTTTCTATGCTCTCCCTGCTGG 90

RESULT 5
US-10-723-860-2812

Sequence 2812, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:

APPLICANT: Aziz, Natasha
APPLICANT: Gineburg, Wendy M.
APPLICANT: Zlocznik, Albert
TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Compositions &
FILE REFERENCE: 05882, 0193, NPO501
CURRENT APPLICATION NUMBER: US/10/723, 860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429, 739
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2812
LENGTH: 1872
TYPE: DNA
ORGANISM: Homo sapiens
US-10-723-860-2812

Query Match 14.2% Score 22; DB 18; Length 1872;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TTTTCTATGCTCTCCCTGCTGG 32
|||||
Db 444 TTTTCTATGCTCTCCCTGCTGG 465

RESULT 6
US-10-037-270-625

Sequence 625, Application US/10037270
Publication No. US20030104529A1
GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundong
APPLICANT: Wang, Danni
APPLICANT: Wang, Zhiwei
APPLICANT: Tillinghaert, John
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030104529A1 Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B

CURRENT APPLICATION NUMBER: US/10/037,270

CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: pf_fl_genes Version 1.0
SEQ ID NO 625
LENGTH: 1878
TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (945)..(1229)
US-10-037-270-625

Query Match 14.2% Score 22; DB 15; Length 1878;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TTTTCTATGCTCTCCCTGCTGG 32
|||||
Db 473 TTTTCTATGCTCTCCCTGCTGG 494

RESULT 7
US-10-117-722-625

Sequence 625, Application US/10117722
Publication No. US20030219744A1
GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030219744A1 Nucleic Acids and
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/10/117,722
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: pf_fl_genes Version 1.0
SEQ ID NO 625
LENGTH: 1878
TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (945)..(1229)
US-10-117-722-625

Query Match 14.2% Score 22; DB 17; Length 1878;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TTTTCTATGCTCTCCCTGCTGG 32
|||||
Db 473 TTTTCTATGCTCTCCCTGCTGG 494

RESULT 8
US-10-723-860-6888

Sequence 6888, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha

APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882, 0193, NPUS01
CURRENT APPLICATION NUMBER: US/10/723, 860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429, 739
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6888
LENGTH: 1894
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (650)..(669)
OTHER INFORMATION: n is a, c, g, or t
US-10-723-860-6888

Query Match 14.2%; Score 22; DB 18; Length 1894;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TTTTCTATGCTCTCCCTGCTGG 32
444 TTTTCTATGCTCTCCCTGCTGG 465

RESULT 9
US-10-198-846-11013

Sequence 11013, Application US/10198846
Publication No. US20030099974A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198, 846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306, 220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11013
LENGTH: 2061
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 1, 2, 3, 1831, 1832, 1833, 1834, 1835, 1836, 1837, 1838,
LOCATION: 1839, 1840, 1841, 1842, 1843, 1844, 1845, 1846, 1847, 1848,
LOCATION: 1849, 1850, 1851, 1852, 1853, 1854, 1855, 1856, 1860, 2009,
LOCATION: 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047
OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc feature
LOCATION: 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057,
LOCATION: 2058, 2059, 2060, 2061
OTHER INFORMATION: n = A,T,C or G
US-10-198-846-11013

Query Match 14.2%; Score 22; DB 14; Length 2061;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TTTTCTATGCTCTCCCTGCTGG 32

DB 436 TTTTCTATGCTCTCCCTGCTGG 457

RESULT 10
US-09-867-701-5894
Sequence 5894, Application US/09867701
Patent No. US20020132237A1
GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121, 497
CURRENT APPLICATION NUMBER: US/09/867, 701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5894
LENGTH: 371
TYPE: DNA
ORGANISM: Homo sapien
US-09-867-701-5894

Query Match 12.9%; Score 20; DB 9; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CTCCTGCTGGCGCTGATG 41
24 CTCCTGCTGGCGCTGATG 43

RESULT 11
US-09-867-701-2415
Sequence 2415, Application US/09867701
Patent No. US20020132237A1
GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121, 497
CURRENT APPLICATION NUMBER: US/09/867, 701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2415
LENGTH: 457
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)....(457)
OTHER INFORMATION: n = A,T,C or G
US-09-867-701-2415

Query Match 12.9%; Score 20; DB 9; Length 457;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 CTCCTGCGCTGATGGAGA 45
32 CTCCTGCGCTGATGGAGA 51

RESULT 12
US-10-273-438-1
Sequence 1, Application US/10273438
Publication No. US20030072757A1
GENERAL INFORMATION:
APPLICANT: Farese, Robert V.

```

; APPLICANT: Cases, Sylvaine
; APPLICANT: Smith, Steven
; GENERAL INFORMATION:
; TITLE OF INVENTION: Diacylglycerol O-Acyltransferase
; FILE REFERENCE: UCAL-105CIP2
; CURRENT APPLICATION NUMBER: US/10/273,438
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US/10/040,315
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/107,771
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/17883
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/103,754
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 09/339,472
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1411
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-273-438-1

Query Match          12.9%; Score 20; DB 14; Length 1411;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 CTCCTGCTGGCGCTGATGG 41
DB 273 CTCCTGCTGGCGCTGATGG 292

RESULT 13
US-10-040-315A-1
; Sequence 1, Application US/10040315A
; Publication No. US20030167483A1
; GENERAL INFORMATION:
; APPLICANT: Farese, Robert V.
; APPLICANT: Cases, Sylvaine
; APPLICANT: Smith, Steven
; APPLICANT: Erickson, Sandra
; TITLE OF INVENTION: Diacylglycerol O-Acyltransferase
; FILE REFERENCE: UCAL-105CIP2
; CURRENT APPLICATION NUMBER: US/10/040,315A
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/107,771
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/17883
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/103,754
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 09/339,472
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1411
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-040-315A-1

Query Match          12.9%; Score 20; DB 16; Length 1411;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 CTCCTGCTGGCGCTGATGG 41
DB 273 CTCCTGCTGGCGCTGATGG 292

RESULT 14
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US-10-659-800-1
; Sequence 1, Application US/10659800
; Publication No. US20040078836A1
; GENERAL INFORMATION:
; APPLICANT: Farese, Robert V.
; APPLICANT: Cases, Sylvaine
; APPLICANT: Smith, Steven
; APPLICANT: Erickson, Sandra
; TITLE OF INVENTION: Diacylglycerol O-Acyltransferase
; FILE REFERENCE: UCAL-105CIP2CON2
; CURRENT APPLICATION NUMBER: US/10/659,800
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/040,315
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/107,771
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/17883
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/103,754
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 09/339,472
; PRIOR FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1411
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-659-800-1

Query Match          12.9%; Score 20; DB 17; Length 1411;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 CTCCTGCTGGCGCTGATGG 41
DB 273 CTCCTGCTGGCGCTGATGG 292

RESULT 15
US-10-278-733-2
; Sequence 2, Application US/10278733
; Publication No. US20030100480A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Steven
; APPLICANT: Chen, Hubert
; APPLICANT: Farese, Robert V Jr
; TITLE OF INVENTION: Methods and compositions for modulating
; FILE REFERENCE: UCAL-105CIP4
; CURRENT APPLICATION NUMBER: US/10/278,733
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: 10/040,315
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/339,472
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/107,771
; PRIOR FILING DATE: 1998-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/17883
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 09/103,754
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1467)
; OTHER INFORMATION: Homo sapiens diacylglycerol O-acyltransferase
; OTHER INFORMATION: homolog 1
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US-10-278-733-2

Query Match 12.9%; Score 20; DB 15; Length 1467;
 Best Local Similarity 100.0%; Pred. No. 0.42;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 CTCCTGCTGCGCTGATGG 41
 Db 579 CTCCTGCTGCGCTGATGG 598

Search completed: February 10, 2005, 00:28:26
 Job time : 275 secs